OM nucleic - nucleic search, using sw model

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GenCore version 5.1.6

Run on: July 31, 2005, 15:46:58 ; Search time 3623.72 Seconds
(without alignments)
777.311 Million cell updates/sec

Title: US-10-041-856-2_COPY_2441_2514
Perfect score: 74
Sequence: 1 atgccaagggaaacttaga.........attcggaagtggttggacaa 74
Scoring table: IDENTITY_NUC
                Gapop 10.0 , Gapext 1.0
Searched: 34239544 seqs, 19032134700 residues
Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   EST:*
        1: gb_est1:*
        2: gb_est2:*
        3: gb_htc:*
        4: gb_est3:*
        5: gb_est4:*
        6: gb_est5:*
        7: gb_est6:*
        8: gb_gss1:*
        9: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	74	100.0	417	7	CN256146	CN256146 170005321
2	74	100.0	447	7	BF840993	BF840993 RC3-HT097
3	74	100.0	513	1	AL702133	AL702133 DKFZp686G
4	74	100.0	580	5	BP243833	BP243833 BP243833
5	74	100.0	603	5	BX478139	BX478139 DKFZp686B
6	74	100.0	618	4	BG395601	BG395601 602458222
7	74	100.0	641	7	BQ807986	BQ807986 NISC_ki2
8	74	100.0	709	7	CN256149	CN256149 170004241
9	74	100.0	803	1	AU124100	AU124100 AU124100
10	74	100.0	866	5	BU508979	BU508979 AGENCOURT
11	74	100.0	874	5	BU156074	BU156074 AGENCOURT
12	74	100.0	931	4	BG286503	BG286503 602382995
13	74	100.0	1134	7	CN641971	CN641971 ILLUMIGEN
14	74	100.0	3833	3	CR749385	CR749385 Homo sapi
15	74	100.0	3999	9	AY414501	AY414501 Homo sapi
16	72.4	97.8	553	7	BM512007	BM512007 ij77d11.x
17	72.4	97.8	713	7	CK833783	CK833783 4057942 B
18	72	83.8	779	4	BG471915	BG471915 60251209
19	62	97.8	911	2	BE256729	BE256729 601115546
20	59.6	80.5	595	5	BQ287640	BQ287640 i67g02.y
21	59.6	80.5	628	7	CN702393	CN702393 E0461G05-
22	59.6	80.5	691	7	CF733016	CF733016 UI-M-HB0-
23	59.6	80.5	731	6	CA317782	CA317782 UI-M-FW0-
24	59.6	80.5	755	7	CF724242	CF724242 UI-M-G20-
25	59.6	80.5	762	7	CN527823	CN527823 UI-M-HQ0-
26	59.6	80.5	779	7	CN532046	CN532046 UI-M-HQ0-
27	59.6	80.5	790	7	CK782242	CK782242 UI-M-HJ0-
28	59.6	80.5	884	5	BQ713281	BQ713281 AGENCOURT
29	59.6	80.5	3083	9	AK035944	AK035944 Mus muscu
30	59.6	80.5	3969	9	AY414503	AY414503 Mus muscu
31	59.6	80.5	4526	3	AK031367	AK031367 Mus muscu
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34	55.4	78.4	579	5	BX854509	BX854509 BX854509
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37	52.2	70.5	824	7	BB575780	BB575780 BB575780
38	50.6	68.4	716	1	AJ739645	AJ739645 AJ739645
39	50.6	68.4	573	1	AJ739639	AJ739639 AJ739639
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41	45.2	61.1	607	7	CN675051	CN675051 A0957H12-
42	41	55.4	591	7	CK897843	CK897843 SGP155016
43	40	54.1	793	7	CN256150	CN256150 170005318
44	39.4	53.2	932	9	AL254552	AL254552 Tetraodon
45	38.6	52.2	1061	9	AL223167	AL223167 Tetraodon

ALIGNMENTS

RESULT 1
CN256146

LOCUS   CN256146   417 bp   mRNA   linear   EST 16-MAY-2004
DEFINITION 1700053218935 GRN_ES Homo sapiens cDNA 5', mRNA sequence.
ACCESSION   CN256146
VERSION   CN256146.1 GI:47272560
KEYWORDS   EST.
SOURCE   Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 417)
AUTHORS   Brandenberger,R., Wei,H., Zhang,S., Lei,S., Murage,J., Fisk,G.J.,
            Li,Y., Xu,C., Fang,R., Guegler,K., Rao,M.S., Mandalam,R.,
            Lebkowski,J. and Stanton,L.W.
TITLE   Transcriptome characterization elucidates signaling networks that
            control human ES cell growth and differentiation
JOURNAL   Nat. Biotechnol. 22 (6), 707-716 (2004)
COMMENT   Contact: Brandenberger R
            Regenerative Medicine
            Geron Corporation
            230 Constitution Drive, Menlo Park, CA 94025, USA
            Tel: 650 473 8658
            Fax: 650 473 7760
            Email: rbrandenberger@geron.com
            Insert Length: 417 Std Error: 0.00.
FEATURES   Location/Qualifiers
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                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone_lib="GRN_ES"
                     /tissue_type="embryonic stem cells, cell lines H1, H7, and
                     H9"
                     /note="oligo dT primed, full-length enriched cDNA library
                     from undifferentiated hES cell lines H1 (p32), H7 (p29),
                     and H9 (p26) maintained in feeder-free conditions"
ORIGIN

Query Match   100.0%; Score 74; DB 7; Length 417;
Best Local Similarity 100.0%; Pred. No. 6.5e-16;
Matches   74; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   1 ATGCCCAAGGGAGGGAAAACTTAGAAGTTGTTCATCATCATCGAGACCCCTGGTTTTTAGCTCAGATTCGG 60
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Db 235 ATGCCCAAGGGAGGGAAAACTTAGAAGTTGTTCATCATCATCGAGACCCCTGGTTTTTAGCTCAGATTCGG 294

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Qy    61 AAGTGGTTGGACAA 74
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Db   295 AAGTGGTTGGACAA 308
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RESULT 2
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LOCUS       BF840993/c
DEFINITION  RC3-HT0974-011200-013-a03 HT0974 Homo sapiens cDNA, mRNA sequence.
ACCESSION   BF840993                447 bp    mRNA    linear   EST 13-JAN-2001
VERSION     BF840993.1  GI:12193641
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 447)
AUTHORS     Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
            Nagai,M.A., da Silva,W.Jr., Zago,M.A., Bordin,S., Costa,F.F.,
            Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
            Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V.,
            O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
            Simpson,A.J.
TITLE       Shotgun sequencing of the human transcriptome with ORF expressed
            sequence tags
JOURNAL     Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
MEDLINE     20202663
PUBMED      10737800
COMMENT     Contact: Simpson A.J.G.
            Laboratory of Cancer Genetics
            Ludwig Institute for Cancer Research
            Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
            Brazil
            Tel: +55-11-2704922
            Fax: +55-11-2707001
            Email: asimpson@ludwig.org.br
            This sequence was derived from the FAPESP/LICR Human Cancer Genome
            Project. This entry can be seen in the following URL
            (http://www.ludwig.org.br/scripts/gethtml2.pl?ti=RC3&t2=RC3-HT0974-
            011200-013-a03&t3=2000-12-01&t4=1)
            Seq_primer: puc 18 forward
            High quality sequence start: 29
            High quality sequence stop: 447.
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                     /db_xref="taxon:9606"
                     /clone_lib="HT0974"
                     /dev_stage="Adult"
                     /clone="RC3-HT0974-011200-013-a03"
                     /note="Organ: head_neck; Vector: puc18; Site_1: SmaI;
                     Site_2: SmaI; A mini-library was made by cloning products
                     derived from ORESTES PCR (U.S. Letters Patent application
                     No. 196,716 - Ludwig Institute for Cancer Research)
                     profiles into the pUC 18 vector. Reverse transcription of
                     tissue mRNA and cDNA amplification were performed under
                     low stringency conditions."
ORIGIN
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Query Match         100.0%;  Score 74;  DB 2;  Length 447;
Best Local Similarity  100.0%;  Pred. No. 6.7e-16;
Matches  74;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;

Qy     1 ATGCCAAGGGGAAACTTAGAAGTTGTTCATCATCGAGCCCCTGGTTTTAGCTCAGATTCGG 60
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Db   268 ATGCCAAGGGGAAACTTAGAAGTTGTTCATCATCGAGCCCCTGGTTTTAGCTCAGATTCGG 209

Qy    61 AAGTGGTTGGACAA 74
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Db   208 AAGTGGTTGGACAA 195
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RESULT 3
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ACCESSION   AL702133
LOCUS       AL702133                513 bp    mRNA    linear   EST 04-SEP-2003
DEFINITION  DKFZp686G02155_r1 686 (synonym: hlcc3) Homo sapiens cDNA clone
            DKFZp686G02155_5', mRNA sequence.
ACCESSION   AL702133
VERSION     AL702133.1  GI:19685488
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 513)
AUTHORS     Wiemann,S.
TITLE       EST (Bloecker,H., Boecher,M., Brandt,P., Mewes,H.W., Weil,B. and
            Wiemann,S.)
JOURNAL     Unpublished (1999)
COMMENT     Contact: MIPS
            MIPS
            Ingolstaeder Landstr.1, D-85764 Neuherberg, Germany
            This is the 5' sequence of the clone insert
            Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
            Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
            sequenced by GBF (National Research Centre for Biotechnology Ltd.,
            Braunschweig/Germany) within the cDNA sequencing consortium of the
            German Genome Project.
            No s1 sequence available.
            This clone (DKFZp686G02155) is available at the RZPD in Berlin.
            Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
            Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.
FEATURES             Location/Qualifiers
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                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="DKFZp686G02155"
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                     /lab_host="DH10B"
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                     /note="Vector: pTriplEx2; Site_1: SfiIA; Site_2: SfiIB;
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ORIGIN
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Query Match         100.0%;  Score 74;  DB 1;  Length 513;
Best Local Similarity  100.0%;  Pred. No. 6.9e-16;
Matches  74;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;

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         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   343 ATGCCAAGGGGAAACTTAGAAGTTGTTCATCATCGAGCCCCTGGTTTTAGCTCAGATTCGG 402

Qy    61 AAGTGGTTGGACAA 74
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Db   403 AAGTGGTTGGACAA 416
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RESULT 4
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LOCUS       BP243833                580 bp    mRNA    linear   EST 15-SEP-2004
DEFINITION  BP243833 Sugano cDNA library, liver HepG2 Homo sapiens cDNA clone
            HEP21727, mRNA sequence.
ACCESSION   BP243833
VERSION     BP243833.1  GI:52116743
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 580)
AUTHORS     Suzuki,Y., Yamashita,R., Shirota,M., Sakakibara,Y., Chiba,J.,
            Mizushima-Sugano,J., Nakai,K. and Sugano,S.
TITLE       Sequence comparison of human and mouse genes reveals a homologous
            block structure in the promoter regions
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OM nucleic - nucleic search, using sw model

GenCore version 5.1.6
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Run on:　　July 31, 2005, 16:38:33 ; Search time 755.531 Seconds
　　　　　　　　　　　　　　　(without alignments)
　　　　　　　　　　　　　　　633.931 Million cell updates/sec

Title:　　　US-10-041-856-2_COPY_2441_2514
Perfect score:　74
Sequence:　1 atgccaagggaaacttaga.........attcggaagtggttggacaa 74

Scoring table:　IDENTITY_NUC
　　　　　　　　　Gapop 10.0 , Gapext 1.0

Searched:　7287783 seqs, 3236178273 residues

Total number of hits satisfying chosen parameters:　14575566

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
　　　　　　　　　Maximum Match 100%
　　　　　　　　　Listing first 45 summaries

Database :　Published Applications NA:*

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2:	/cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*						
3:	/cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*						
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7:	/cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq:*						
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SUMMARIES

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1	74	100.0	117	13	US-10-050-189A-10	Sequence 10, Appl
2	74	100.0	4256	20	US-10-719-993-319	Sequence 319, App
3	74	100.0	4803	10	US-09-930-213-276	Sequence 276, App
4	74	100.0	4803	21	US-10-956-157-1094	Sequence 1094, Ap
5	74	100.0	5840	20	US-10-719-993-322	Sequence 322, App
6	74	100.0	5924	13	US-10-041-856-2	Sequence 2, Appli
7	74	100.0	5957	20	US-10-719-993-320	Sequence 320, App

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

8	74	100.0	6107	20	US-10-719-993-321	Sequence 321, App
9	74	100.0	6179	20	US-10-719-993-318	Sequence 318, App
10	74	100.0	6479	13	US-10-041-856-1	Sequence 1, Appli
11	74	100.0	6863	20	US-10-719-993-6863	Sequence 6863, Ap
12	57	100.0	78878	20	US-10-719-993-499	Sequence 4499, Ap
13	57	77.0	201	20	US-10-719-993-4499	Sequence 4499, Ap
14	57	77.0	201	20	US-10-719-993-4527	Sequence 4527, Ap
15	57	77.0	201	20	US-10-719-993-4556	Sequence 4556, Ap
16	57	77.0	201	20	US-10-719-993-4585	Sequence 4585, Ap
17	27.6	77.0	1899	17	US-10-282-1222A-24563	Sequence 24563, A
18	27	36.5	201	20	US-10-719-993-34903	Sequence 34903, A
19	26.6	35.9	941	20	US-10-005-057A-38	Sequence 38, Appl
20	26.6	35.9	941	18	US-10-675-072A-5	Sequence 5, Appli
21	26.4	35.7	1855	19	US-10-437-963-100577	Sequence 100577,
22	26.4	35.7	4320	19	US-10-630-518-17	Sequence 17, Appl
23	26	35.1	4320	19	US-10-630-518-21	Sequence 21, Appl
24	25.8	34.9	2920	22	US-10-739-930-898	Sequence 898, App
25	25.8	34.9	600	20	US-09-972-079-76053	Sequence 76053, A
26	25.8	34.8	1563	9	US-09-938-842A-672	Sequence 672, App
27	25.8	34.6	1563	11	US-09-938-842A-672	Sequence 672, App
28	25.6	34.6	484	19	US-10-872-156-34	Sequence 34, Appl
29	25.6	34.6	201	20	US-10-719-993-52377	Sequence 52377, A
30	25.6	34.6	186854	19	US-10-437-963-63832	Sequence 63832, A
31	25.6	34.6	248436	13	US-10-087-192-2014	Sequence 2014, Ap
32	25.6	34.4	339926	20	US-10-719-993-7048	Sequence 7048, Ap
33	25.4	34.3	96289	19	US-10-322-281-211	Sequence 211, App
34	25.4	34.1	535	20	US-10-363-345A-32723	Sequence 32723, A
35	25.2	34.1	535	20	US-10-363-345A-32723	Sequence 32723, A
36	25.2	34.1	535	20	US-10-363-483A-32724	Sequence 32724, A
37	25.2	34.1	617	19	US-10-363-483A-32724	Sequence 32724, A
38	25.2	34.1	617	13	US-10-027-632-244158	Sequence 244158,
39	25.2	34.1	617	17	US-10-027-632-244158	Sequence 244158,
40	25.2	34.1	3186778	13	US-10-027-632-174961	Sequence 174961,
41	25.2	34.1	3186778	17	US-10-027-632-174961	Sequence 174961,
42	25	33.8	981	10	US-09-822-846-282	Sequence 282, App
43	25	33.8	1811	10	US-09-822-846-283	Sequence 283, App
44	25	33.8	2666	20	US-10-425-115-51127	Sequence 51127, A
45	24.8	33.5	600	22	US-10-972-079-35597	Sequence 35597, A

ALIGNMENTS

RESULT 1
US-10-050-189A-10
Sequence 10, Application US/10050189A
; Publication No. US20020168656A1
; GENERAL INFORMATION:
; APPLICANT: Rubin, Berish
; APPLICANT: Anderson, Sylvia
; TITLE OF INVENTION: Detection of Mutations in a Gene Encoding IKB Kinase-Complex-Asso
; TITLE OF INVENTION: Protein to Diagnose Familial Dysautonomia
; FILE REFERENCE: Rubin 2.0
; CURRENT APPLICATION NUMBER: US/10/050,189A
; CURRENT FILING DATE: 2002-01-16
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 10
; LENGTH: 117
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-050-189A-10

　Query Match　　　100.0%;
　Best Local Similarity　100.0%;
　Matches　74;　Conservative　0;

　　　　Score 74;　DB 13;　Length 117;
　　　　Pred. No. 3.1e-18;
　　　　Mismatches　0;　Indels　0;　Gaps　0;

Qy　　1 ATGCCAAGGGAAACTTAGAAGTTGTTCATCATCGAGCCCTTGGTTTTTAGCTTCAGATTCGG 60
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Qy　　61 AAGTGGTTGGACAA 74
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Db　　61 AAGTGGTTGGACAA 74

Db   88 AAGTGGTTGGACAA 101

RESULT 2
US-10-719-993-319
; Sequence 319, Application US/10719993
; Publication No. US20040265849A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: ALZHEIMER'S DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001496
; CURRENT APPLICATION NUMBER: US/10/719,993
; CURRENT FILING DATE: 2003-11-24
; NUMBER OF SEQ ID NOS: 55342
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 319
; LENGTH: 4256
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-719-993-319

Query Match   100.0%; Score 74; DB 20; Length 4256;
Best Local Similarity   100.0%; Pred. No. 1.1e-17;
Matches   74; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   1 ATGCCAAGGGGGAAACTTAGAAGTTGTTCATCATCGAGCCCTGGGTTTTAGCTCAGATTCGG 60
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Qy   61 AAGTGGTTGGACAA 74
          ||||||||||||||
Db   2551 AAGTGGTTGGACAA 2564

RESULT 3
US-09-930-213-276
; Sequence 276, Application US/09930213
; Publication No. US20030170625A1
; GENERAL INFORMATION:
; APPLICANT: ROSENTHAL, ANDRE
; APPLICANT: HINZMANN, BERND
; APPLICANT: SCHAFER, REINHARD
; APPLICANT: ZUBER, JOHANNES
; APPLICANT: TCHE-NITSE, OLEG
; APPLICANT: GRIPS, MARTIN
; APPLICANT: HELLNEGEL, MARTIN
; APPLICANT: SCHMITZ, ANNE-CHANTAL
; APPLICANT: SERS, CHRISTINE
; TITLE OF INVENTION: DETECTION OF DIFFERENTIAL GENE EXPRESSIONS
; FILE REFERENCE: ALBRE-14
; CURRENT APPLICATION NUMBER: US/09/930,213
; CURRENT FILING DATE: 2001-01-31
; PRIOR APPLICATION NUMBER: DE 10004102.7
; PRIOR FILING DATE: 2000-01-31
; NUMBER OF SEQ ID NOS: 885
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 276
; LENGTH: 4803
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-930-213-276

Query Match   100.0%; Score 74; DB 10; Length 4803;
Best Local Similarity   100.0%; Pred. No. 1.1e-17;
Matches   74; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   1 ATGCCAAGGGGGAAACTTAGAAGTTGTTCATCATCGAGCCCTGGGTTTTAGCTCAGATTCGG 60
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Db   2434 ATGCCAAGGGGGAAACTTAGAAGTTGTTCATCATCGAGCCCTGGGTTTTAGCTCAGATTCGG 2493

Qy   61 AAGTGGTTGGACAA 74
          ||||||||||||||
Db   2494 AAGTGGTTGGACAA 2507

Db   2494 AAGTGGTTGGACAA 2507

RESULT 4
US-10-956-157-1094
; Sequence 1094, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 1094
; LENGTH: 4803
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-956-157-1094

Query Match   100.0%; Score 74; DB 21; Length 4803;
Best Local Similarity   100.0%; Pred. No. 1.1e-17;
Matches   74; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   1 ATGCCAAGGGGGAAACTTAGAAGTTGTTCATCATCGAGCCCTGGGTTTTAGCTCAGATTCGG 60
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Db   2434 ATGCCAAGGGGGAAACTTAGAAGTTGTTCATCATCGAGCCCTGGGTTTTAGCTCAGATTCGG 2493

Qy   61 AAGTGGTTGGACAA 74
          ||||||||||||||
Db   2494 AAGTGGTTGGACAA 2507

RESULT 5
US-10-719-993-322
; Sequence 322, Application US/10719993
; Publication No. US20040265849A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: ALZHEIMER'S DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001496
; CURRENT APPLICATION NUMBER: US/10/719,993
; CURRENT FILING DATE: 2003-11-24
; NUMBER OF SEQ ID NOS: 55342
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 322
; LENGTH: 5840
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-719-993-322

Query Match   100.0%; Score 74; DB 20; Length 5840;
Best Local Similarity   100.0%; Pred. No. 1.2e-17;
Matches   74; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   1 ATGCCAAGGGGGAAACTTAGAAGTTGTTCATCATCGAGCCCTGGGTTTTAGCTCAGATTCGG 60
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Db   2491 ATGCCAAGGGGGAAACTTAGAAGTTGTTCATCATCGAGCCCTGGGTTTTAGCTCAGATTCGG 2550

Qy   61 AAGTGGTTGGACAA 74
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Db   2551 AAGTGGTTGGACAA 2564

RESULT 6
US-10-041-856-2
; Sequence 2, Application US/10041856
; Publication No. US20020169299A1
; GENERAL INFORMATION:

OM nucleic - nucleic search, using sw model

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GenCore version 5.1.6

Run on: July 31, 2005, 14:44:02 ; Search time 2130.01 Seconds
(without alignments)
1683.411 Million cell updates/sec

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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
Searched: 4708233 seqs, 2422607955 residues
Total number of hits satisfying chosen parameters: 9416466
Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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2: gb_htg:*
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4: gb_om:*
5: gb_ov:*
6: gb_pat:*
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9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vi:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	74	100.0	117	6	AX481363	AX481363 Sequence
2	74	100.0	803	6	BD147310	BD147310 Primer fo
3	74	100.0	803	6	AX867248	AX867248 Sequence
4	74	100.0	2471	6	BD157787	BD157787 Primer fo
5	74	100.0	2471	6	AX879348	AX879348 Sequence
6	74	100.0	2471	6	AK022559	AK022559 Homo sapi
7	74	100.0	3516	6	CQ724004	CQ724004 Sequence
8	74	100.0	3999	6	AR070165	AR070165 Sequence
9	74	100.0	3999	6	AR124807	AR124807 Sequence
10	74	100.0	4417	6	CQ850139	CQ850139 Sequence
11	74	100.0	4417	6	AK127237	AK127237 Homo sapi
12	74	100.0	4788	6	BD156525	BD156525 Primer fo
13	74	100.0	4788	6	AX877177	AX877177 Sequence
14	74	100.0	4788	6	AK001641	AK001641 Homo sapi
15	74	100.0	4803	6	BD171366	BD171366 Method fo
16	74	100.0	4803	6	BD173600	BD173600 Method of
17	74	100.0	4803	6	AX210634	AX210634 Sequence
18	74	100.0	4803	6	AF044195	AF044195 Homo sapi
19	74	100.0	5047	9	BC033094	BC033094 Homo sapi
20	74	100.0	5924	6	AX676049	AX676049 Sequence
21	74	100.0	5924	9	AF153419	AF153419 Homo sapi
22	74	100.0	66479	6	AX676048	AX676048 Sequence
23	74	100.0	78376	9	AL359692	AL359692 Human DNA
24	69.2	93.5	4347	4	AF388202	AF388202 Oryctolag
25	59.6	80.5	4645	10	AF388201	AF388201 Rattus no
26	59.6	80.5	4765	10	BC052387	BC052387 Mus muscu
27	59.6	80.5	4799	10	AF367244	AF367244 Mus muscu
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30	59.6	80.5	224915	2	AC096902	AC096902 Rattus no
31	59.6	80.5	264321	10	AL807762	AL807762 Mouse DNA
32	59.6	68.4	4169	5	AJ720452	AJ720452 Gallus ga
33	50.6	48.4	128177	2	BX927373	BX927373 Danio rer
34	30.8	41.6	160516	10	AL928943	AL928943 Mouse DNA
35	29.2	39.5	2535	3	AK173465	AK173465 Ciona int
36	29	39.2	68661	3	AC024805	AC024805 Caenorhab
37	29	39.2	278007	2	AC006799	AC006799 Caenorhab
38	28.2	38.1	181644	9	AL139350	AL139350 Human DNA
39	27.8	37.6	181585	9	AC104989	AC104989 Homo sapi
40	27.6	37.3	8868	3	CEY32B12A	CEY32B12A Caenorhab
41	27.6	37.3	222204	2	AC126953	AC126953 Rattus no
42	27.6	37.3	224499	14	AF482758	AF482758 Cowpox vi
43	27.6	37.3	324050	1	AL591983	AL591983 Listeria
44	27.6	37.3	349980	1	AX641671	AX641671 Sequence
45	27.6	37.3	349980	6	AX641672	AX641672 Sequence

ALIGNMENTS

RESULT 1
AX481363
LOCUS   AX481363   117 bp   DNA   linear   PAT 16-AUG-2002
DEFINITION Sequence 10 from Patent EP1225232.
ACCESSION   AX481363
VERSION   AX481363.1 GI:22316284
KEYWORDS
SOURCE   Homo sapiens (human)
  ORGANISM Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Rubin,B.Y. and Anderson,S.L.
  TITLE   Detection of mutations in a gene encoding Ikappab
            kinase-complex-associated protein to diagnose familial dysautonomia
  JOURNAL   Patent: EP 1225232-A 10 24-JUL-2002;
            Rubin, Berish Y. (US) ; Anderson, Silvia L. (US)
FEATURES   Location/Qualifiers
     source   1..117
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
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Query Match   100.0%; Score 74; DB 6; Length 117;
Best Local Similarity   100.0%; Pred. No. 1.3e-17;
Matches   74; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

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Db   28 ATGCCAAGGGAAACTTAGAAGTTGTTCATCATCGAGCGCCCTGGTTTTTTAGCTCAGATTCGG 87

Qy   61 AAGTGGTTGGACAA 74
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Db   88 AAGTGGTTGGACAA 101

RESULT 2
BD147310
LOCUS   BD147310   803 bp   DNA   linear   PAT 17-JAN-2003
DEFINITION Primer for synthesizing full-length cDNA and use thereof.
ACCESSION   BD147310

VERSION   BD147310.1 GI:27853068
KEYWORDS   JP 200291363-A/2153.
SOURCE   Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 803)
  AUTHORS   Ota,T., Isogai,T., Nishikawa,T., Hayashi,K., Saito,K., Yamamoto,J.,
            Ishii,S., Sugiyama,T., Wakamatsu,A., Nagai,K. and Otsuki,T.
  TITLE   Primer for synthesizing full-length cDNA and use thereof.
  JOURNAL   Patent: JP 200291363-A 2153 09-JUL-2002;
            HELIX RESEARCH INSTITUTE
COMMENT   PN   JP 200291363-A/2153
            PD   09-JUL-2002
            PF   28-JUL-2000 JP 2000280990
            PI   TOSHIO OTA,TAKAO ISOGAI,TETSUO NISHIKAWA,KOJI HAYASHI,KAORU
            PI   SAITO,
            PI   JUNICHI YAMAMOTO,SHIZUKO ISHII,TOMOYASU SUGIYAMA,AI WAKAMATSU,
            PI   KEIICHI NAGAI,TETSUJI OTSUKI
            PC   C12N15/09,C07K14/47,C07K16/18,C12N1/15,C12N1/19,C12N1/21,C12N5/ PC
            PC   10,
            PC   C12P21/02,C12Q1/68//C12P21/08,G06F17/30,C12N15/00,C12N5/00 CC
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                     /organism="Homo sapiens"
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                     /db_xref="taxon:9606"
ORIGIN

Query Match   100.0%; Score 74; DB 6; Length 803;
  Best Local Similarity 100.0%; Pred. No. 1.8e-17;
  Matches 74; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy   1 ATGCCAAGGGGAAACTTAGAAGTTGTTCATCATCCGAGCCCTGGGTTTTAGCTCAGATTCGG 60
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Db 123 ATGCCAAGGGGAAACTTAGAAGTTGTTCATCATCCGAGCCCTGGGTTTTAGCTCAGATTCGG 182

Qy   61 AAGTGGTTGGACAA 74
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Db 183 AAGTGGTTGGACAA 196

RESULT 3
LOCUS   AX867248   803 bp   DNA   linear   PAT 17-DEC-2003
DEFINITION Sequence 2153 from Patent EP1074617.
ACCESSION   AX867248
VERSION   AX867248.1 GI:40021619
KEYWORDS
SOURCE   Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Ota,T., Isogai,T., Nishikawa,T., Hayashi,K., Saito,K., Yamamoto,J.,
            Ishii,S., Sugiyama,T., Wakamatsu,A., Nagai,K. and Otsuki,T.
  TITLE   Primers for synthesizing full-length cDNA and their use
  JOURNAL   Patent: EP 1074617-A 2153 07-FEB-2001;
            Research Association for Biotechnology (JP)
FEATURES   Location/Qualifiers
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                     /mol_type="unassigned DNA"
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ORIGIN

Query Match   100.0%; Score 74; DB 6; Length 803;

RESULT 4
LOCUS   BD157787   2471 bp   DNA   linear   PAT 17-JAN-2003
DEFINITION Primer for synthesizing full-length cDNA and use thereof.
ACCESSION   BD157787
VERSION   BD157787.1 GI:27863545
KEYWORDS   JP 200291363-A/12630.
SOURCE   Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 2471)
  AUTHORS   Ota,T., Isogai,T., Nishikawa,T., Hayashi,K., Saito,K., Yamamoto,J.,
            Ishii,S., Sugiyama,T., Wakamatsu,A., Nagai,K. and Otsuki,T.
  TITLE   Primer for synthesizing full-length cDNA and use thereof
  JOURNAL   Patent: JP 200291363-A 12630 09-JUL-2002;
            HELIX RESEARCH INSTITUTE
COMMENT   PN   JP 200291363-A/12630
            PD   09-JUL-2002
            PF   28-JUL-2000 JP 2000280990
            PI   TOSHIO OTA,TAKAO ISOGAI,TETSUO NISHIKAWA,KOJI HAYASHI,KAORU
            PI   SAITO,
            PI   JUNICHI YAMAMOTO,SHIZUKO ISHII,TOMOYASU SUGIYAMA,AI WAKAMATSU,
            PI   KEIICHI NAGAI,TETSUJI OTSUKI
            PC   C12N15/09,C07K14/47,C07K16/18,C12N1/15,C12N1/19,C12N1/21,C12N5/ PC
            PC   10,
            PC   C12P21/02,C12Q1/68//C12P21/08,G06F17/30,C12N15/00,C12N5/00 CC
            Primer for synthesizing full-length cDNA and use thereof FH Key
            FT   CDS   (772)..(1989).
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ORIGIN

Query Match   100.0%; Score 74; DB 6; Length 2471;
  Best Local Similarity 100.0%; Pred. No. 2.1e-17;
  Matches 74; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy   1 ATGCCAAGGGGAAACTTAGAAGTTGTTCATCATCCGAGCCCTGGGTTTTAGCTCAGATTCGG 60
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Db 123 ATGCCAAGGGGAAACTTAGAAGTTGTTCATCATCCGAGCCCTGGGTTTTAGCTCAGATTCGG 182

Qy   61 AAGTGGTTGGACAA 74
         ||||||||||||||
Db 183 AAGTGGTTGGACAA 196

RESULT 5
LOCUS   AX879348   14253 bp   DNA   linear   PAT 17-DEC-2003
DEFINITION Sequence 14253 from Patent EP1074617.
ACCESSION   AX879348
VERSION   AX879348.1 GI:40034084
KEYWORDS
SOURCE   Homo sapiens (human)
ORGANISM   Homo sapiens

OM nucleic - nucleic search, using sw model

GenCore version 5.1.6
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Run on: July 31, 2005, 09:42:59 ; Search time 523.938 Seconds
836.092 Million cell updates/sec
(without alignments)

Title: US-10-041-856-2_COPY_2441_2514
Perfect score: 74
Sequence: 1 atgccaagggaaacttaga.........attcggaagtggttggacaa 74
Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
Searched: 4390206 seqs, 2959870667 residues
Total number of hits satisfying chosen parameters: 8780412

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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13: geneseqn2004bs:*

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	74	100.0	117	6	ABN84790	Abn84790 IkappaB k
2	74	100.0	803	4	AAH05318	Aah05318 Human CDN
3	74	100.0	2471	4	AAH15795	Aah15795 Human CDN
4	74	100.0	3999	2	AAX28025	Aax28025 Human IKA
5	74	100.0	3999	4	AAF29756	Aaf29756 Human IKA
6	74	100.0	4417	13	ADR07102	Adr07102 Full leng
7	74	100.0	4788	4	AAH14533	Aah14533 Human CDN
8	74	100.0	4803	5	AAH81767	Aah81767 Human dif
9	74	100.0	4803	6	AAL44190	Aal44190 Human I-k
10	74	100.0	5924	6	ABQ80570	Abq80570 Mutant hu
11	74	100.0	5924	6	ABQ80569	Abq80569 Human IKB
12	74	100.0	5924	8	ACD13384	Acd13384 Human DNA
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16	74	100.0	6479	6	ABQ80565	Abq80565 Human IKB
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18	27.6	80.5	645	10	ACA36693	Aca36693 Prokaryot
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c 21	26.6	35.9	941	6	ABQ75916	Abq75916 CHD activ
c 22	26.4	35.7	4320	6	AAL48977	Aal48977 A thalian
c 23	25.8	35.6	1008	10	ADE90065	Ade90065 Human rho
c 24	25.8	34.9	1563	3	AAC43257	Aac43257 Arabidops
c 25	25.8	34.9	1563	6	AB212867	Ab212867 A. thalia
c 26	25.8	34.9	1563	6	ADG87872	Adg87872 A. thalia
c 27	25.8	34.9	1563	6	ADG88134	Adg88134 A. thalia
c 28	25.8	34.9	2252	4	AB121828	Ab121828 Drosophil
c 29	25.8	34.9	2384	4	AB121864	Ab121864 Drosophil
c 30	25.6	34.6	248436	11	ACN45190	Acn45190 Human gen
c 31	25.4	34.3	792	4	AB116845	Ab116845 Drosophil
c 32	25.4	34.3	2792	4	AB116844	Ab116844 Drosophil
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c 36	25.2	34.1	535	6	ABQ46132	Abq46132 Oligonucl
c 37	25.2	34.1	535	6	ABQ46133	Abq46133 Oligonucl
c 38	25.2	34.1	5623	4	ABL18300	Abl18300 Drosophil
c 39	25	33.8	981	6	ABK35891	Abk35891 cDNA sequ
c 40	25	33.8	1811	6	ABK35892	Abk35892 cDNA sequ
c 41	25	33.8	3474	12	ADQ62997	Adq62997 Novel hum
c 42	25	33.8	109973	3	AAF22298	Aaf22298 BAC conta
c 43	24.8	33.5	1244	4	AAH73111	Aah73111 Human cer
c 44	24.8	33.5	1244	4	AAH73113	Aah73113 Human cer
c 45	24.8	33.5	194883	11	ACN44398	Acn44398 Human gen

ALIGNMENTS

RESULT 1
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ID   ABN84790 standard; cDNA; 117 BP.
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AC   ABN84790;
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DT   05-NOV-2002 (first entry)
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DE   Ikappa kinase-complex-associated protein exon 19-21 sequence.
XX
KW   Familial dysautonomia; Riley-Day syndrome;
KW   hereditary sensory neuropathy III; human; carrier; diagnosis;
KW   IkappaB kinase-complex associated protein; IKAP; chromosome 9q31; gene;
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OS   Homo sapiens.
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FT   /product= "IKAP peptide"
FT   /note= "the CDS does not include a start or stop codon"
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PN   EP1225232-A2.
XX
PD   24-JUL-2002.
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PF   17-JAN-2002; 2002EP-00001232.
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PR   17-JAN-2001; 2001US-0262284P.
XX
PA   (RUBI/) RUBIN B Y.
PA   (ANDE/) ANDERSON S L.
XX
PI   Rubin BY, Anderson SL;
XX
DR   WPI; 2002-601228/65.
DR   P-PSDB; ABB79767.
XX
PT   Detecting a polymorphism in a gene encoding the IkappaB kinase-complex-
PT   associated protein is used to diagnose and identify carriers of familial
PT   dysautonomia.

XX
PS Disclosure; Fig 1B; 16pp; English.
XX
CC The present sequence comprises cDNA corresponding to exons 19-21 of the
CC IkappaB kinase complex-associated protein (IKAP) gene of an individual
CC unaffected by familial dysautonomia (FD). It was obtained by PCR
CC amplification using the primers given in ABN84788-89. Alignment of this
CC sequence with that from an FD-affected individual (see ABN84791)
CC indicated that exclusion of exon 20 in the RNA transcribed from the FD
CC allele resulted in a frameshift, causing premature termination of
CC translation and a protein truncated by 619 amino acids. Normal IKAP has
CC 1332 amino acids. The invention provides a method for detecting a
CC polymorphism linked to a gene associated with FD. This allows the
CC diagnosis of FD and the identification of carriers. It involves detecting
CC a disruptive mutation in a gene encoding IKAP on chromosome 9q31. The
CC mutation is a T to C transition in position 6 of the donor splice site of
CC intron 20 and/or a G to C transversion of nucleotide 2390 in exon 19 of
CC the IKAP gene
XX
SQ Sequence 117 BP; 35 A; 22 C; 29 G; 31 T; 0 U; 0 Other;

Qy Query Match 100.0%; Score 74; DB 6; Length 117;
    Best Local Similarity 100.0%; Pred. No. 6.2e-18;
    Matches 74; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db  28 ATGCCAAGGGGAAAACTTAGAAGTTGTTCATCATCGAGCCCTGGGTTTTAGCTCAGAATTCGG 87

Qy  61 AAGTGGTTGGACAA 74
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Db  88 AAGTGGTTGGACAA 101
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RESULT 2
AAH05318
ID AAH05318 standard; cDNA; 803 BP.
XX
AC AAH05318;
XX
DT 26-JUN-2001 (first entry)
XX
DE Human cDNA clone (5'-primer) SEQ ID NO:2153.
XX
KW Human; primer; detection; diagnosis; antisense therapy; gene therapy; ss.
XX
OS Homo sapiens.
XX
PN EP1074617-A2.
XX
PD 07-FEB-2001.
XX
PF 28-JUL-2000; 2000EP-00116126.
XX
PR 29-JUL-1999; 99JP-00248036.
PR 27-AUG-1999; 99JP-00300253.
PR 11-JAN-2000; 2000JP-00187776.
PR 02-MAY-2000; 2000JP-00183767.
PR 09-JUN-2000; 2000JP-00241899.
XX
PA (HELI-) HELIX RES INST.
XX
PI Ota T, Isogai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J;
PI Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T;
XX
DR WPI; 2001-318749/34.
XX
PT Primer sets for synthesizing polynucleotides, particularly the 5602 full-
PT length cDNAs defined in the specification, and for the detection and/or
PT diagnosis of the abnormality of the proteins encoded by the full-length
PT cDNAs.
XX
PS Claim 1; SEQ ID NO 2153; 2537pp + Sequence Listing; English.

XX
CC The present invention describes primer sets for synthesising 5602 full-
CC length cDNAs defined in the specification. Where a primer set comprises:
CC (a) an oligo-dT primer and an oligonucleotide complementary to the
CC complementary strand of a polynucleotide which comprises one of the 5602
CC nucleotide sequences defined in the specification, where the
CC oligonucleotide comprises at least 15 nucleotides; or (b) a combination
CC of an oligonucleotide comprising a sequence complementary to the
CC complementary strand of a polynucleotide which comprises a 5'-end
CC sequence and an oligonucleotide comprising a sequence complementary to a
CC polynucleotide which comprises a 3'-end sequence, where the
CC oligonucleotide comprises at least 15 nucleotides and the combination of
CC the 5'-end sequence/3'-end sequence is selected from those defined in the
CC specification. The primer set can be used in antisense therapy and in
CC gene therapy. The primers are useful for synthesising polynucleotides,
CC particularly full-length cDNAs. The primers are also useful for the
CC detection and/or diagnosis of the abnormality of the proteins encoded by
CC the full-length cDNAs. The primers allow obtaining of the full-length
CC cDNAs easily without any specialised methods. AAH03166 to AAH13628 and
CC AAH13633 to AAH18742 represent human amino acid sequences; AAB92446 and
CC AAH13629 to AAH13632 represent
CC oligonucleotides; all of which are used in the exemplification of the
CC present invention
XX
SQ Sequence 803 BP; 251 A; 154 C; 172 G; 222 T; 0 U; 4 Other;

Qy Query Match 100.0%; Score 74; DB 4; Length 803;
    Best Local Similarity 100.0%; Pred. No. 1.1e-17;
    Matches 74; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db  123 ATGCCAAGGGGAAAACTTAGAAGTTGTTCATCATCGAGCCCTGGGTTTTAGCTCAGAATTCGG 182

Qy  61 AAGTGGTTGGACAA 74
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Db  183 AAGTGGTTGGACAA 196
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RESULT 3
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ID AAH15795 standard; cDNA; 2471 BP.
XX
AC AAH15795;
XX
DT 26-JUN-2001 (first entry)
XX
DE Human cDNA sequence SEQ ID NO:14253.
XX
KW Human; primer; detection; diagnosis; antisense therapy; gene therapy; ss.
XX
OS Homo sapiens.
XX
PN EP1074617-A2.
XX
PD 07-FEB-2001.
XX
PF 28-JUL-2000; 2000EP-00116126.
XX
PR 29-JUL-1999; 99JP-00248036.
PR 27-AUG-1999; 99JP-00300253.
PR 11-JAN-2000; 2000JP-00187776.
PR 02-MAY-2000; 2000JP-00183767.
PR 09-JUN-2000; 2000JP-00241899.
XX
PA (HELI-) HELIX RES INST.
XX
PI Ota T, Isogai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J;
PI Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T;
XX
DR WPI; 2001-318749/34.
XX
PT Primer sets for synthesizing polynucleotides, particularly the 5602 full-

OM nucleic - nucleic search, using sw model

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Run on: July 31, 2005, 14:57:07 ; Search time 153.025 Seconds
                 (without alignments)
                 791.274 Million cell updates/sec

Title: US-10-041-856-2_COPY_2441_2514
Perfect score: 74
Sequence: 1 atgccaagggaaacttaga.........attcggaagtggttggacaa 74

Scoring table: IDENTITY_NUC
                 Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818118359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
                  Maximum Match 100%
                  Listing first 45 summaries

Database :   Issued_Patents_NA:*
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             2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
             3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
             4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
             5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
             6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	74	100.0	3999	2	US-08-971-244-1	Sequence 1, Appli
2	74	100.0	3999	2	US-09-286-891-1	Sequence 1, Appli
3	25.8	34.9	343352	4	US-09-949-016-13498	Sequence 13498, A
4	25	33.8	601	4	US-09-949-016-124821	Sequence 124821,
5	25	33.8	19302	4	US-09-949-016-15270	Sequence 15270, A
6	24.8	33.5	178888	4	US-09-949-016-12733	Sequence 12733, A
7	24.8	33.2	178884	4	US-09-949-016-13039	Sequence 13039, A
8	24.6	33.2	650	4	US-09-270-767-26023	Sequence 26023, A
9	24.6	33.2	1816	4	US-09-270-767-10593	Sequence 10593, A
10	24.4	33.0	572	4	US-09-513-999C-3823	Sequence 3823, Ap
11	24.2	32.7	2634	4	US-09-799-451-784	Sequence 784, Appl
12	24.2	32.7	6719	3	US-09-740-235-36	Sequence 36, Appl
13	24.2	32.7	8021	3	US-09-740-235-2	Sequence 2, Appli
14	24	32.4	601	4	US-09-949-016-45487	Sequence 45487, A
15	24	32.4	2412	4	US-09-583-110-553	Sequence 553, App
16	24	32.4	2421	4	US-09-107-433-2039	Sequence 2039, Ap
17	24	32.4	21706	3	US-08-961-527-36	Sequence 36, Appl
18	23.8	32.2	102409	4	US-09-949-016-15148	Sequence 15148, A
19	23.6	31.9	243	4	US-09-540-236-1400	Sequence 1400, Ap
20	23.6	31.9	1535	4	US-09-949-016-12826	Sequence 12826, Ap
21	23.6	31.9	1535	4	US-09-949-016-12827	Sequence 12827, A
22	23.6	31.9	1535	4	US-09-949-016-12828	Sequence 12828, A
23	23.6	31.9	1535	4	US-09-949-016-12829	Sequence 12829, A
24	23.6	31.9	1536	4	US-09-949-016-13366	Sequence 13366, A
25	23.6	31.9	1536	4	US-09-949-016-13367	Sequence 13367, A
26	23.6	31.9	1536	4	US-09-949-016-13368	Sequence 13368, A
27	23.6	31.9	1536	4	US-09-949-016-13369	Sequence 13369, A
28	23.6	31.9	94877	4	US-09-949-016-16114	Sequence 16114, A
29	23.6	31.9	276687	4	US-09-949-016-13840	Sequence 13840, A
30	23.6	31.9	346112	4	US-09-949-016-13165	Sequence 13165, A
31	23.4	31.6	540	4	US-09-270-767-9718	Sequence 9718, A
32	23.4	31.6	540	4	US-09-270-767-25000	Sequence 25000, A
33	23.4	31.6	601	4	US-09-949-016-174274	Sequence 174274,
34	23.4	31.6	601	4	US-09-949-016-174275	Sequence 174275,
35	23.4	31.6	601	4	US-09-949-016-174466	Sequence 174466,
36	23.4	31.6	601	4	US-09-949-016-174467	Sequence 174467,
37	23.4	31.6	972	4	US-09-134-000C-2123	Sequence 2123, Ap
38	23.4	31.6	2990	3	US-09-009-816-19	Sequence 19, Appl
39	23.4	31.6	3093	4	US-09-949-016-5131	Sequence 5131, Ap
40	23.4	31.6	126237	4	US-09-949-016-16674	Sequence 16674, A
41	23.4	31.6	126237	4	US-09-949-016-16675	Sequence 16675, A
42	23.2	31.4	601	4	US-09-949-016-86782	Sequence 86782, A
43	23.2	31.4	601	4	US-09-949-016-89263	Sequence 89263, A
44	23.2	31.4	601	4	US-09-949-016-89264	Sequence 89264, A
45	23.2	31.4	2967	3	US-08-637-823B-26	Sequence 26, Appl

ALIGNMENTS

RESULT 1
US-08-971-244-1

; Sequence 1, Application US/08971244
; Patent No. 5891719
; GENERAL INFORMATION:
; APPLICANT: Cohen, Lucy
; APPLICANT: Baeuerle, Patrick
; TITLE OF INVENTION: IKAP Proteins, Nucleic Acids and Methods
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
; STREET: 75 DENISE DRIVE
; CITY: HILLSBOROUGH
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94010
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/971,244
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: OSMAN, RICHARD A
; REGISTRATION NUMBER: 36,627
; REFERENCE/DOCKET NUMBER: T97-011
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 343-4342
; TELEFAX: (650) 343-4341
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3999 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..3996
US-08-971-244-1

Query Match 100.0%; Score 74; DB 2; Length 3999;
Best Local Similarity 100.0%; Pred. No. 2.7e-19;
Matches 74 Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy   1 ATGCCAAGGGAAACTTAGAAGTTGTTCATCATCGAGCCCTGGTTTTAGCTCAGATTCGG 60
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Db   2131 ATGCCAAGGGGAAACTTAGAAGTTGTTCATCATCGAGCCCTGGGTTTTTTAGCTTCAGATTCGG 2190
Qy   61 AAGTGGTTGGACAA 74
          ||||||||||||||
Db   2191 AAGTGGTTGGACAA 2204

RESULT 2
US-09-286-891-1
; Sequence 1, Application US/09286891
; Patent No. 6172195
; GENERAL INFORMATION:
; APPLICANT: Cohen, Lucy
; APPLICANT: Baeuerle, Patrick
; TITLE OF INVENTION: IKAP Proteins, Nucleic Acids and Methods
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
; STREET: 75 DENISE DRIVE
; CITY: HILLSBOROUGH
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94010
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/286,891
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/971,244
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: OSMAN, RICHARD A
; REGISTRATION NUMBER: 36,627
; REFERENCE/DOCKET NUMBER: T97-011
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 343-4342
; TELEFAX: (650) 343-4341
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3999 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..3996

Query Match   100.0%; Score 74; DB 3; Length 3999;
Best Local Similarity 100.0%;
Matches   74; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

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Db   2131 ATGCCAAGGGGAAACTTAGAAGTTGTTCATCATCGAGCCCTGGTTTTTTAGCTCAGATTCGG 2190

Qy   61 AAGTGGTTGGACAA 74
          ||||||||||||||
Db   2191 AAGTGGTTGGACAA 2204

RESULT 3
US-09-949-016-13498/c
; Sequence 13498, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.

; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 13498
; LENGTH: 343352
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(343352)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-13498

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Best Local Similarity 63.9%; Pred. No. 32;
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Qy   68 T 68
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Db 11204 T 11204

RESULT 4
US-09-949-016-124821/c
; Sequence 124821, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 124821
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-124821

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Db   586 TGCTAAGAGGAAATTTCTAATGTTTTCAACACAAAACTATGGATTAGTAGTATCATATTCCAC 527

Qy   62 AGTGGTTGGACAA 74
          ||| || ||
Db   526 ATTGTTATTTAGAA 514

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OM nucleic - nucleic search, using sw model

Run on: July 31, 2005, 15:46:58 ; Search time 734.537 Seconds
(without alignments)
777.311 Million cell updates/sec

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Perfect score:   15
Sequence:        1 aagtaagyccatg 15
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Searched:        34239544 seqs, 19032134700 residues
Total number of hits satisfying chosen parameters:   68479088

Minimum DB seq length: 0
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                 Maximum Match 100%
                 Listing first 45 summaries

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                 6: gb_est5:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.		Score	% Query Match	Length	DB	ID	Description
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c	3	14.6	97.3	456	1	AI492486	AI492486 ti28e08-x
c	4	14.6	97.3	458	1	AI492495	AI492495 ti28f07.x
c	5	14.6	97.3	550	4	BM582147	BM582147 17006872
c	6	14.6	97.3	668	5	BQ407386	BQ407386 GA_Ed010
c	7	14.6	97.3	679	5	BX313682	BX313682
c	8	14.6	97.3	737	9	CE603670	CE603670 tigr-gss-
c	9	14.6	97.3	749	7	CK937519	CK937519 CGF10477
c	10	14.6	97.3	841	7	CN202392	CN202392 Tor2548 G
c	11	14.6	97.3	848	2	BE570328	BE570328 60133209
c	12	14.6	97.3	905	1	AI348093	AI348093 qp61g11.x
c	13	13.6	90.7	164	8	AZ463592	AZ463592 1M027H01
c	14	13.6	90.7	235	1	AV033029	AV033029
c	15	13.6	90.7	252	8	BF773503	BF773503 CM2-IT003
c	16	13.6	90.7	262	8	AZ554007	AZ554007 RPCI-23-2
c	17	13.6	90.7	280	4	BM570636	BM570636 i104f01.Y
c	18	13.6	90.7	282	4	BG234760	BG234760 dab63f11.
c	19	13.6	90.7	291	9	BX243232	BX243232 Danio rer
c	20	13.6	90.7	304	6	CD410777	CD410777 Gm_ck3908
c	21	13.6	90.7	319	8	AZ234490	AZ234490 RPCI-23-8
c	22	13.6	90.7	341	8	BY214916	BY214916 RPCI-23-8
c	23	13.6	90.7	341	7	CK519547	CK519547 rsweao_00
c	24	13.6	90.7	348	2	BE637256	BE637256 WHE1295-1
c	25	13.6	90.7	351	5	BY324268	BY324268
c	26	13.6	90.7	360	8	AZ768375	AZ768375 1M056BP13
c	27	13.6	90.7	360	9	CC592729	CC592729 CH240_393
c	28	13.6	90.7	373	9	CR111055	CR111055 Reverse s
c	29	13.6	90.7	389	7	CK300936	CK300936 UI-E-EJ1-
c	30	13.6	90.7	392	4	BI750496	BI750496 Ta01_08d1
c	31	13.6	90.7	404	8	AZ231614	AZ231614 RPCI-23-9
c	32	13.6	90.7	410	9	CW524034	CW524034 OP_Ba004
c	33	13.6	90.7	413	8	AQ076964	AQ076964 CIT-HSP-2
c	34	13.6	90.7	431	8	AQ518681	AQ518681 HS 5085 B
c	35	13.6	90.7	433	8	AZ707731	AZ707731 RPCI-23-2
c	36	13.6	90.7	446	2	BB845860	BB845860 23684 BA
c	37	13.6	90.7	475	8	AZ289694	AZ289694 RPCI-23-1
c	38	13.6	90.7	482	6	CA590184	CA590184 hab23a07.
c	39	13.6	90.7	496	4	BI449178	BI449178 dab99h05.
c	40	13.6	90.7	503	2	AW603835	AW603835 CM0-CN004
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c	42	13.6	90.7	518	1	AL694388	AL694388
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c	44	13.6	90.7	521	8	AZ237823	AZ237823 RPCI-23-7
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ALIGNMENTS

RESULT 1
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LOCUS       BG221595                273 bp    mRNA    linear   EST 21-APR-2001
DEFINITION  RST41409 Atherys RAGE Library Homo sapiens cDNA, mRNA sequence.
ACCESSION   BG221595
VERSION     BG221595.1  GI:13747616
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 273)
AUTHORS     Harrington,J.J., Sherf,B., Rundlett,S., Jackson,P.D., Perry,R.,
            Cain,S., Leventhal,C., Thornton,M., Ramachandran,R.,
            Whittington,J., Lerner,L., Costanzo,D., McElligott,K., Boozer,S.,
            Mays,R., Smith,E., Veloso,N., Klika,A., Hess,J., Cothren,K., Lo,K.,
            Offenbacher,J., Danzig,J. and Ducar,M.
TITLE       Creation of genome-wide protein expression libraries using random
            activation of gene expression
JOURNAL     Nat. Biotechnol. 19 (5), 440-445 (2001)
MEDLINE     21227151
PUBMED      11329013
COMMENT     Contact: Scott J. Cain
            Athersys, Inc.
            3201 Carnegie Ave, Cleveland, OH 44115, USA
            Tel: 216 431 9900
            Fax: 216 361 9596
            Email: scain@athersys.com
            High quality sequence stop: 223.
FEATURES             Location/Qualifiers
     source          1..273
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                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
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                     /clone_lib="Athersys RAGE Library"
                     /note="See 'Creation of Genome-wide Protein Expression
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                     Nature Biotechnology, in press. Note that even though the
                     cell type indicated is HT1080, since a random activation
                     method was used, these sequence tags are not necessarily
                     expressed in HT1080 under normal circumstances."
ORIGIN

Query Match             97.3%;  Score 14.6;  DB 4;  Length 273;
Best Local Similarity   93.3%;  Pred. No. 1.2e+03;
Matches   14;  Conservative   1;  Mismatches   0;  Indels   0;  Gaps   0;
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RESULT 2

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Db   52 AAGTAAAGCCCATG 38
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LOCUS   AQ168111   354 bp   DNA   linear   GSS 16-OCT-1998
DEFINITION HS_2233_A1_F07_MF CIT Approved Human Genomic Sperm Library D Homo
            sapiens genomic clone Plate=2233 Col=13 Row=K, genomic survey
            sequence.
ACCESSION   AQ168111
VERSION   AQ168111.1   GI:3561746
KEYWORDS   GSS.
SOURCE   Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 354)
AUTHORS   Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,
            Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and
            Hood,L.
TITLE   Sequence-tagged connectors: A sequence approach to mapping and
            scanning the human genome
JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
MEDLINE   99380589
PUBMED   10449764
COMMENT   Contact: Mahairas GG, Wallace JC, Hood L
            High Throughput Sequencing Center
            University of Washington
            401 Queen Anne Avenue North, Seattle, WA 98109, USA
            Tel: (206) 616-3618
            Fax: (206) 616-3887
            Email: jwallace@u.washington.edu
            Sequence Tagged Connector
            Plate: 2233 row: K column: 13
            Class: BAC ends
            High quality sequence stop: 354.
FEATURES   Location/Qualifiers
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             /organism="Homo sapiens"
             /mol_type="genomic DNA"
             /db_xref="taxon:9606"
             /clone="Plate=2233 Col=13 Row=K"
             /sex="male"
             /clone_lib="CIT Approved Human Genomic Sperm Library D"
             /note="Organ: sperm; Vector: pBeloBAC11; BAC Clones in
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ORIGIN
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Query Match    97.3%;    Score 14.6;    DB 8;    Length 354;
Best Local Similarity    93.3%;    Pred. No. 1.2e+03;
Matches    14;    Conservative    1;    Mismatches    0;    Indels    0;    Gaps    0;

REFERENCE   1  (bases 1 to 456)
AUTHORS     NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE       National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
JOURNAL     Unpublished (1997)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
            Emmert-Buck, M.D., Ph.D.
            cDNA Library Preparation: M. Bento Soares, Ph.D.
            cDNA Library Arrayed by: Greg Lennon, Ph.D.
            DNA Sequencing by: Washington University Genome Sequencing Center
            Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html
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            High quality sequence stop: 451.
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             /mol_type="mRNA"
             /db_xref="taxon:9606"
             /clone="IMAGE:2131814"
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             /lab_host="DH10B"
             /note="Organ: kidney; Vector: pT7T3D-Pac (Pharmacia) with
             a modified polylinker; Site_1: Not I; Site_2: Eco RI;
             plasmid DNA from the normalized library NCI_CGAP_Kid3 was
             prepared, and ss circles were made in vitro. Following HAP
             purification, this DNA was used as tracer in a subtractive
             hybridization reaction. The driver was PCR-amplified cDNAs
             from a pool of 5,000 clones made from the same library
             (cloneIDs 1322376-1323911, 1456007-1456775, and
             1500552-1502855). Subtraction by Bento Soares and M.
             Fatima Bonaldo."
ORIGIN

RESULT 3

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Qy    1 AAGTAAGYGCCATTG 15
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Db  262 AAGTAAGTGCCATG 276
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Query Match   97.3%;   Score 14.6;   DB 8;   Length 354;
Best Local Similarity   93.3%;   Pred. No. 1.2e+03;
Matches   14;   Conservative   1;   Mismatches   0;   Indels   0;   Gaps   0;

LOCUS   AI492486/c
DEFINITION AI492486   456 bp   mRNA   linear   EST 30-MAR-1999
            ti28e08.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2131814 3'
            similar to contains MER7.t3 MER7 repetitive element ;, mRNA
            sequence.
ACCESSION   AI492486
VERSION   AI492486.1   GI:4393489
KEYWORDS   EST.
SOURCE   Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

RESULT 4

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Qy    1 AAGTAAGYGCCATTG 15
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Db  271 AAGTAAGTGCCATG 257
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Query Match   97.3%;   Score 14.6;   DB 1;   Length 456;
Best Local Similarity   93.3%;   Pred. No. 1.3e+03;
Matches   14;   Conservative   1;   Mismatches   0;   Indels   0;   Gaps   0;

LOCUS   AI492495/c
DEFINITION AI492495   458 bp   mRNA   linear   EST 30-MAR-1999
            ti28f07.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2131813 3'
            similar to contains MER7.t3 MER7 MER7 repetitive element ;, mRNA
            sequence.
ACCESSION   AI492495
VERSION   AI492495.1   GI:4393498
KEYWORDS   EST.
SOURCE   Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 458)
AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE   National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
JOURNAL   Unpublished (1997)
COMMENT   Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: M. Bento Soares, Ph.D.
            Emmert-Buck, M.D., Ph.D.
            cDNA Library Preparation: Christopher Moskaluk, M.D., Ph.D., Michael R.
            cDNA Library Arrayed by: Greg Lennon, Ph.D.
            DNA Sequencing by: Washington University Genome Sequencing Center
            Clone distribution: NCI-CGAP clone distribution information can be

OM nucleic - nucleic search, using sw model

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

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Post-processing : Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Perfect score: 15
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Gapop 10.0 , Gapext 1.0
Searched: 1202784 seqs, 818183359 residues

Database : Issued_Patents_NA:*
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Minimum DB seq length: 0
Maximum DB seq length: 200000000

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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1	14.6	97.3	246240	2	US-08-724-394A-20	Sequence 20, Appl
2	14.6	97.3	246240	2	US-08-724-394A-21	Sequence 21, Appl
3	14.6	97.3	246240	2	US-08-724-394A-22	Sequence 22, Appl
4	13.6	90.7	390	3	US-09-134-000C-1436	Sequence 1436, Ap
5	13.6	90.7	430	3	US-09-280-116-233	Sequence 233, App
6	13.6	90.7	601	4	US-09-949-016-34133	Sequence 34133, A
7	13.6	90.7	601	4	US-09-949-016-85899	Sequence 85899, A
8	13.6	90.7	601	4	US-09-949-016-130381	Sequence 130381,
9	13.6	90.7	1020	3	US-08-913-264-3	Sequence 3, Appli
10	13.6	90.7	2360	3	US-08-913-264-12	Sequence 12, Appl
11	13.6	90.7	3105	4	US-09-543-681A-4000	Sequence 4000, Ap
12	13.6	90.7	7355	4	US-09-900-920-1	Sequence 1, Appli
13	13.6	90.7	13417	2	US-08-637-759B-37	Sequence 37, Appl
14	13.6	90.7	13417	3	US-08-871-355A-37	Sequence 37, Appl
15	13.6	90.7	13417	3	US-09-201-945-37	Sequence 37, Appl
16	13.6	90.7	50000	4	US-09-146-053-3	Sequence 3, Appli
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22	13.2	88.0	601	4	US-09-949-016-130382	Sequence 130382,
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24	13	86.7	601	4	US-09-949-016-57865	Sequence 57865, A
25	13	86.7	601	4	US-09-949-016-57866	Sequence 57866, A
26	13	86.7	601	4	US-09-949-016-78824	Sequence 78824, A
27	13	86.7	601	4	US-09-949-016-90072	Sequence 90072, A
28	13	86.7	601	4	US-09-949-016-90073	Sequence 90073, A
29	13	86.7	601	4	US-09-949-016-90074	Sequence 90074, A
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31	13	86.7	601	4	US-09-949-016-120318	Sequence 120318,
32	13	86.7	601	4	US-09-949-016-123965	Sequence 123965,
33	13	86.7	601	4	US-09-949-016-171546	Sequence 171546,
34	13	86.7	601	4	US-09-949-016-199187	Sequence 199187,
35	13	86.7	614	3	US-09-280-116-71	Sequence 71, Appl
36	13	86.7	747	4	US-08-956-171B-650	Sequence 650, App
37	13	86.7	747	4	US-08-781-986A-650	Sequence 650, App
38	13	86.7	918	3	US-09-134-001C-2201	Sequence 2201, Ap
39	13	86.7	918	4	US-09-711-164-223	Sequence 223, App
40	13	86.7	1001	4	US-09-671-317-424	Sequence 424, App
41	13	86.7	1470	4	US-09-328-352-1204	Sequence 1204, Ap
42	13	86.7	1555	3	US-08-747-574-3	Sequence 3, Appli
43	13	86.7	1615	4	US-09-220-002-1	Sequence 1, Appli
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ALIGNMENTS

RESULT 1
US-08-724-394A-20/c
; Sequence 20, Application US/08724394A
; Patent No. 5872237
; GENERAL INFORMATION:
; APPLICANT: Feder, John N.
; APPLICANT: Kronmal, Gregory S.
; APPLICANT: Lauer, Peter M.
; APPLICANT: Ruddy, David A.
; APPLICANT: Thomas, Winston
; APPLICANT: Tsuchihashi, Zenta
; APPLICANT: Wolff, Roger K.
; TITLE OF INVENTION: Megabase Transcript Map: No. 5872237el
; TITLE OF INVENTION: Sequences and Antibodies Thereto
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/724,394A
; FILING DATE: 01-OCT-1996
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Fitts, Renee A.
; REGISTRATION NUMBER: 35,136
; REFERENCE/DOCKET NUMBER: 017957-000100
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-576-0200
; TELEFAX: 415-576-0300
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 246240 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 1..246240
; OTHER INFORMATION: /note= "HLA-H.CONTIG"
US-08-724-394A-20

Query Match   97.3%;   Score 14.6; DB 2;   Length 246240;
Best Local Similarity   93.3%;   Pred. No. 1.2e+02;
Matches   14; Conservative   1; Mismatches   0; Indels   0; Gaps   0;

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RESULT 2
US-08-724-394A-21/c
; Sequence 21, Application US/08724394A
; Patent No. 5872237
; GENERAL INFORMATION:
;   APPLICANT: Feder, John N.
;   APPLICANT: Kronmal, Gregory S.
;   APPLICANT: Lauer, Peter M.
;   APPLICANT: Ruddy, David A.
;   APPLICANT: Thomas, Winston
;   APPLICANT: Tsuchihashi, Zenta
;   APPLICANT: Wolff, Roger K.
;   TITLE OF INVENTION: Megabase Transcript Map: No. 5872237el
;   TITLE OF INVENTION: Sequences and Antibodies Thereto
;   NUMBER OF SEQUENCES: 31
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP
;   STREET: Two Embarcadero Center, 8th Floor
;   CITY: San Francisco
;   STATE: CA
;   COUNTRY: USA
;   ZIP: 94111-3834
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: PatentIn Release #1.0, Version #1.30
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/08/724,394A
;   FILING DATE: 01-OCT-1996
;   CLASSIFICATION: 536
;   ATTORNEY/AGENT INFORMATION:
;   NAME: Fitts, Renee A.
;   REGISTRATION NUMBER: 35,136
;   REFERENCE/DOCKET NUMBER: 017957-000100
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE: 415-576-0200
;   TELEFAX: 415-576-0300
; INFORMATION FOR SEQ ID NO: 21:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 246240 base pairs
;   TYPE: nucleic acid
;   STRANDEDNESS: not relevant
;   TOPOLOGY: not relevant
;   MOLECULE TYPE: cDNA
;   FEATURE:
;   NAME/KEY: misc feature
;   LOCATION: 1..246240
;   OTHER INFORMATION: /note= "HLA-H.CONTIG"
US-08-724-394A-21

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Best Local Similarity   93.3%;   Pred. No. 1.2e+02;
Matches   14; Conservative   1; Mismatches   0; Indels   0; Gaps   0;

Qy   1 AAGTAAGYGCCATTG 15
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Db   155908 AAGTAAGTGCCATTG 155894

RESULT 3
US-08-724-394A-22/c
; Sequence 22, Application US/08724394A

; Patent No. 5872237
; GENERAL INFORMATION:
;   APPLICANT: Feder, John N.
;   APPLICANT: Kronmal, Gregory S.
;   APPLICANT: Lauer, Peter M.
;   APPLICANT: Ruddy, David A.
;   APPLICANT: Thomas, Winston
;   APPLICANT: Tsuchihashi, Zenta
;   APPLICANT: Wolff, Roger K.
;   TITLE OF INVENTION: Megabase Transcript Map: No. 5872237el
;   TITLE OF INVENTION: Sequences and Antibodies Thereto
;   NUMBER OF SEQUENCES: 31
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP
;   STREET: Two Embarcadero Center, 8th Floor
;   CITY: San Francisco
;   STATE: CA
;   COUNTRY: USA
;   ZIP: 94111-3834
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: PatentIn Release #1.0, Version #1.30
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/08/724,394A
;   FILING DATE: 01-OCT-1996
;   CLASSIFICATION: 536
;   ATTORNEY/AGENT INFORMATION:
;   NAME: Fitts, Renee A.
;   REGISTRATION NUMBER: 35,136
;   REFERENCE/DOCKET NUMBER: 017957-000100
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE: 415-576-0200
;   TELEFAX: 415-576-0300
; INFORMATION FOR SEQ ID NO: 22:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 246240 base pairs
;   TYPE: nucleic acid
;   STRANDEDNESS: not relevant
;   TOPOLOGY: not relevant
;   MOLECULE TYPE: cDNA
;   FEATURE:
;   NAME/KEY: misc feature
;   LOCATION: 1..246240
;   OTHER INFORMATION: /note= "HLA-H.CONTIG"
US-08-724-394A-22

Query Match   97.3%;   Score 14.6; DB 2;   Length 246240;
Best Local Similarity   93.3%;   Pred. No. 1.2e+02;
Matches   14; Conservative   1; Mismatches   0; Indels   0; Gaps   0;

Qy   1 AAGTAAGYGCCATTG 15
             |||||||:||||||||
Db   155908 AAGTAAGTGCCATTG 155894

RESULT 4
US-09-134-000C-1436/c
; Sequence 1436, Application US/09134000C
; Patent No. 6617156
; GENERAL INFORMATION:
;   APPLICANT: Lynn Doucette-Stamm et al
;   TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
;   TITLE OF INVENTION: ENTEROCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS
;   FILE REFERENCE: 032796-032
;   CURRENT APPLICATION NUMBER: US/09/134,000C
;   CURRENT FILING DATE: 1998-08-13
;   PRIOR APPLICATION NUMBER: US 60/055,778
;   PRIOR FILING DATE: 1997-08-15
;   NUMBER OF SEQ ID NOS: 6812
;   SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1436

OM nucleic - nucleic search, using sw model

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Total number of hits satisfying chosen parameters: 14575566

Post-processing: Minimum Match 0%
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Minimum DB seq length: 0
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Database :   Published_Applications_NA:*

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c	12:	13.6	90.7	/cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*
c	13:	13.6	90.7	/cgn2_6/ptodata/1/pubpna/US0A_PUBCOMB.seq:*
c	14:	13.6	90.7	/cgn2_6/ptodata/1/pubpna/US0B_PUBCOMB.seq:*
c	15:	13.6	90.7	/cgn2_6/ptodata/1/pubpna/US0C_PUBCOMB.seq:*
c	16:	13.6	90.7	/cgn2_6/ptodata/1/pubpna/US0D_PUBCOMB.seq:*
c	17:	13.6	90.7	/cgn2_6/ptodata/1/pubpna/US0E_PUBCOMB.seq:*
c	18:	13.6	90.7	/cgn2_6/ptodata/1/pubpna/US0F_PUBCOMB.seq:*
c	19:	13.6	90.7	/cgn2_6/ptodata/1/pubpna/US0G_PUBCOMB.seq:*
c	20:	13.6	90.7	/cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*
c	21:	13.6	90.7	/cgn2_6/ptodata/1/pubpna/US10I_PUBCOMB.seq:*
c	22:	13.6	90.7	/cgn2_6/ptodata/1/pubpna/US10_PUBCOMB.seq:*
c	23:	13.6	90.7	/cgn2_6/ptodata/1/pubpna/US11A_PUBCOMB.seq:*
c	24:	13.6	90.7	/cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq:*
c	25:	13.6	90.7	/cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*
c	26:	13.6	90.7	/cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

c	8	14.6	97.3	721	17	US-10-027-632-32791	Sequence 32791, A
c	9	14.6	97.3	1139	19	US-10-437-963-67889	Sequence 67889, A
c	10	14.6	97.3	66479	13	US-10-041-856-1	Sequence 1, Appli
c	11	14.6	97.3	78878	20	US-10-719-993-6863	Sequence 6863, Ap
c	12	14.6	97.3	235033	15	US-10-301-844-1	Sequence 776, App
c	13	14.6	97.3	237326	21	US-10-301-844-2	Sequence 2, Appli
c	14	13.6	90.7	25	15	US-10-956-157-171767	Sequence 171767,
c	15	13.6	90.7	25	21	US-10-956-157-267777	Sequence 267777,
c	16	13.6	90.7	25	22	US-10-719-956-106967	Sequence 106967,
c	17	13.6	90.7	228	17	US-10-398-221-17492	Sequence 17492, A
c	18	13.6	90.7	422	19	US-10-767-701-17492	Sequence 17492, A
c	19	13.6	90.7	541	13	US-10-027-632-115092	Sequence 115092,
c	20	13.6	90.7	541	13	US-10-027-632-115093	Sequence 115093,
c	21	13.6	90.7	541	13	US-10-027-632-115094	Sequence 115094,
c	22	13.6	90.7	541	17	US-10-027-632-115092	Sequence 115092,
c	23	13.6	90.7	541	17	US-10-027-632-115093	Sequence 115093,
c	24	13.6	90.7	541	17	US-10-027-632-115094	Sequence 115094,
c	25	13.6	90.7	566	20	US-10-425-115-116253	Sequence 116253,
c	26	13.6	90.7	570	10	US-10-425-115-116253	Sequence 116253,
c	27	13.6	90.7	595	10	US-09-840-743-58	Sequence 58, Appl
c	28	13.6	90.7	600	21	US-09-840-743-68	Sequence 68, Appl
c	29	13.6	90.7	600	22	US-10-956-157-10380	Sequence 10380, A
c	30	13.6	90.7	609	13	US-10-027-079-28919	Sequence 28919, A
c	31	13.6	90.7	609	13	US-10-027-632-85666	Sequence 85666, A
c	32	13.6	90.7	609	17	US-10-027-632-303182	Sequence 303182,
c	33	13.6	90.7	609	17	US-10-027-632-303182	Sequence 303182,
c	34	13.6	90.7	706	19	US-10-437-963-35749	Sequence 35749, A
c	35	13.6	90.7	751	21	US-10-487-901-17508	Sequence 17508, Ap
c	36	13.6	90.7	1305	19	US-10-437-963-2628	Sequence 2628, Ap
c	37	13.6	90.7	1309	20	US-10-425-115-177687	Sequence 177687,
c	38	13.6	90.7	1446	21	US-10-469-204-90	Sequence 90, Appl
c	39	13.6	90.7	1453	9	US-09-070-927A-246	Sequence 246, App
c	40	13.6	90.7	1592	20	US-10-425-115-177698	Sequence 177698,
c	41	13.6	90.7	1592	21	US-10-425-115-5145	Sequence 5145, Ap
c	42	13.6	90.7	1953	9	US-10-956-157-5145	Sequence 5145, Ap
c	43	13.6	90.7	1957	9	US-09-864-761-16018	Sequence 16018, A
c	44	13.6	90.7	2162	21	US-10-684-129-25	Sequence 25, Appl
c	45	13.6	90.7	2173	21	US-10-684-129-11	Sequence 11, Appl
	45	13.6	90.7	2175	21	US-10-684-129-28	Sequence 28, Appl

ALIGNMENTS

RESULT 1
US-10-041-856-85
; Sequence 85, Application US/10041856
; Publication No. US20020169299A1
; GENERAL INFORMATION:
; APPLICANT: SLAUGENHAUPT, SUSAN
; APPLICANT: GUSELLA, JAMES F.
; TITLE OF INVENTION: GENE FOR IDENTIFYING INDIVIDUALS WITH FAMILIAL
; TITLE OF INVENTION: DYSAUTONOMIA
; FILE REFERENCE: 1829-4004US1
; CURRENT APPLICATION NUMBER: US/10/041,856
; CURRENT FILING DATE: 2002-07-08
; PRIOR APPLICATION NUMBER: 60/260,080
; PRIOR FILING DATE: 2001-01-06
; NUMBER OF SEQ ID NOS: 88
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 85
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Probe
US-10-041-856-85

  Query Match   97.3%;
  Best Local Similarity   100.0%;
  Matches   15;   Conservative   0;

Qy   1 AAGTAAGYGCCATTG 15
            |||||||||||||||
          1 AAGTAAGYGCCATTG 15

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	14.6	97.3	15	13	US-10-041-856-85	Sequence 85, Appl
2	14.6	97.3	201	20	US-10-719-993-34903	Sequence 34903, A
3	14.6	97.3	369	21	US-10-487-901-3816	Sequence 3816, Ap
4	14.6	97.3	593	21	US-10-487-901-4354	Sequence 4354, Ap
5	14.6	97.3	721	13	US-10-027-632-32790	Sequence 32790, A
6	14.6	97.3	721	13	US-10-027-632-32791	Sequence 32791, A
7	14.6	97.3	721	17	US-10-027-632-32790	Sequence 32790, A

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

  Score 14.6;   DB 13;   Length 15;
  Pred. No. 1.9e+02;
  Mismatches   0;   Indels   0;   Gaps   0;

Db 1 AAGTAAGYGCCATTG 15

RESULT 2
US-10-719-993-34903
; Sequence 34903, Application US/10719993
; Publication No. US20040258849A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: ALZHEIMER'S DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001496
; CURRENT APPLICATION NUMBER: US/10/719,993
; CURRENT FILING DATE: 2003-11-24
; NUMBER OF SEQ ID NOS: 55342
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 34903
; LENGTH: 201
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-719-993-34903

Query Match 97.3%; Score 14.6; DB 20; Length 201;
Best Local Similarity 93.3%; Pred. No. 2.6e+02;
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAGTAAGYGCCATTG 15
   ||||||||:||||||
Db 26 AAGTAAGTGCCATTG 40

RESULT 3
US-10-487-901-3816/c
; Sequence 3816, Application US/10487901
; Publication No. US20050091708A1
; GENERAL INFORMATION:
; APPLICANT: Oreido, Jeremiah Vincent
; APPLICANT: McCrery, David
; APPLICANT: Pell, Randy
; APPLICANT: Miller, Barbara
; APPLICANT: Weglarz, Thaddeus
; APPLICANT: Gachotte, Daniel
; APPLICANT: Blakeslee, Beth
; APPLICANT: Larrinua, Ignacio
; APPLICANT: Reddy, Avutu
; APPLICANT: Shukla, Vipula
; APPLICANT: Crosley, Rodney
; TITLE OF INVENTION: Nucleic Acid Compositions Conferring Altered Metabolic Characteri
; FILE REFERENCE: DOW-08552
; CURRENT APPLICATION NUMBER: US/10/487,901
; CURRENT FILING DATE: 2004-02-26
; NUMBER OF SEQ ID NOS: 7560
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3816
; LENGTH: 369
; TYPE: DNA
; ORGANISM: Trichoderma harzianum
US-10-487-901-3816

Query Match 97.3%; Score 14.6; DB 21; Length 369;
Best Local Similarity 93.3%; Pred. No. 2.8e+02;
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAGTAAGYGCCATTG 15
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Db 43 AAGTAAGCGCCATTG 29

RESULT 4
US-10-487-901-4354/c
; Sequence 4354, Application US/10487901
; Publication No. US20050091708A1
; GENERAL INFORMATION:

; APPLICANT: Oreido, Jeremiah Vincent
; APPLICANT: McCrery, David
; APPLICANT: Pell, Randy
; APPLICANT: Miller, Barbara
; APPLICANT: Weglarz, Thaddeus
; APPLICANT: Gachotte, Daniel
; APPLICANT: Blakeslee, Beth
; APPLICANT: Larrinua, Ignacio
; APPLICANT: Reddy, Avutu
; APPLICANT: Shukla, Vipula
; APPLICANT: Crosley, Rodney
; TITLE OF INVENTION: Nucleic Acid Compositions Conferring Altered Metabolic Characteri
; FILE REFERENCE: DOW-08552
; CURRENT APPLICATION NUMBER: US/10/487,901
; CURRENT FILING DATE: 2004-02-26
; NUMBER OF SEQ ID NOS: 7560
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4354
; LENGTH: 593
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-487-901-4354

Query Match 97.3%; Score 14.6; DB 21; Length 593;
Best Local Similarity 93.3%; Pred. No. 2.9e+02;
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAGTAAGYGCCATTG 15
   ||||||||:||||||
Db 264 AAGTAAGCGCCATTG 250

RESULT 5
US-10-027-632-32790/c
; Sequence 32790, Application US/10027632
; Publication No. US20020198371A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; TITLE OF INVENTION: Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 32790
; LENGTH: 721
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-32790

Query Match 97.3%; Score 14.6; DB 13; Length 721;
Best Local Similarity 93.3%; Pred. No. 3e+02;
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAGTAAGYGCCATTG 15
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OM nucleic - nucleic search, using sw model

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GenCore version 5.1.6

Run on: July 31, 2005, 14:57:07 ; Search time 31.0185 Seconds
(without alignments)
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Title: US-10-041-856-86
Perfect score: 15
Sequence: 1 ggttcacsgattgtc 15
Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 81818359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents NA:*
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2: /cgn2_6/ptcdata/1/ina/5B_COMB.seq:*
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4: /cgn2_6/ptcdata/1/ina/6B_COMB.seq:*
5: /cgn2_6/ptcdata/1/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptcdata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	14.6	97.3	3999	2	US-08-971-244-1	Sequence 1, Appli
2	14.6	97.3	3999	3	US-09-286-891-1	Sequence 1, Appli
3	13.6	90.7	798	3	US-09-270-767-13909	Sequence 13909, A
4	13	86.7	242	4	US-09-270-767-28047	Sequence 28047, A
5	13	86.7	347	4	US-09-270-767-12302	Sequence 12302, A
6	13	86.7	675	4	US-09-252-991A-2680	Sequence 2680, Ap
7	13	86.7	1092	4	US-09-252-991A-2996	Sequence 2996, Ap
8	13	86.7	2544	4	US-09-252-991A-2775	Sequence 2775, Ap
9	13	86.7	2691	4	US-09-252-991A-3187	Sequence 3187, Ap
10	13	86.7	3162	4	US-09-356-643B-12	Sequence 12, Appl
11	13	86.7	3162	4	US-10-053-510-12	Sequence 12, Appl
12	13	86.7	38343	4	US-09-949-016-15714	Sequence 15714, A
13	13	86.7	818128	4	US-09-949-016-14546	Sequence 14546, A
14	13	86.7	818128	4	US-09-949-016-14547	Sequence 14547, A
15	13	86.7	818128	4	US-09-949-016-14548	Sequence 14548, A
16	13	86.7	818128	4	US-09-949-016-14549	Sequence 14549, A
17	13	86.7	818128	4	US-09-949-016-14550	Sequence 14550, A
18	13	86.7	818128	4	US-09-949-016-14551	Sequence 14551, A
19	13	86.7	818128	4	US-09-949-016-14552	Sequence 14552, A
20	13	86.7	818128	4	US-09-949-016-14553	Sequence 14553, A
21	13	86.7	818128	4	US-09-949-016-14554	Sequence 14554, A
22	13	86.7	818128	4	US-09-949-016-14555	Sequence 14555, A
23	13	86.7	818128	4	US-09-949-016-14556	Sequence 14556, A
24	13	86.7	818128	4	US-09-949-016-14557	Sequence 14557, A
25	13	86.7	818128	4	US-09-949-016-14558	Sequence 14558, A
26	13	86.7	818128	4	US-09-949-016-14559	Sequence 14559, A
27	13	86.7	818128	4	US-09-949-016-14560	Sequence 14560, A
28	13	86.7	818128	4	US-09-949-016-14561	Sequence 14561, A
29	13	86.7	818128	4	US-09-949-016-14562	Sequence 14562, A
30	13	86.7	818128	4	US-09-949-016-14564	Sequence 14564, A
31	13	86.7	818128	4	US-09-949-016-14565	Sequence 14565, A
32	13	86.7	818128	4	US-09-949-016-14566	Sequence 14566, A
33	13	86.7	818128	4	US-09-949-016-14567	Sequence 14567, A
34	12.6	84.0	601	4	US-09-949-016-88086	Sequence 88086, A
35	12.6	84.0	756	4	US-09-949-016-88	Sequence 88, Appl
36	12.6	84.0	756	4	US-09-270-767-15370	Sequence 15370, A
37	12.6	84.0	837	3	US-09-134-001C-814	Sequence 814, App
38	12.6	84.0	1434	4	US-09-540-236-1750	Sequence 1750, Ap
39	12.6	84.0	1492	3	US-09-196-520-7	Sequence 7, Appli
40	12.6	84.0	1772	4	US-09-311-021-139	Sequence 139, App
41	12.6	84.0	1923	4	US-09-328-352-3932	Sequence 3932, App
42	12.6	84.0	2307	4	US-09-328-352-276	Sequence 276, App
43	12.6	84.0	3675	4	US-09-107-532A-2566	Sequence 2566, Ap
44	12.6	84.0	4224	4	US-09-328-352-3759	Sequence 3759, Ap
45	12.6	84.0	8797	4	US-09-949-016-16186	Sequence 16186, A

ALIGNMENTS

RESULT 1
US-08-971-244-1
; Sequence 1, Application US/08971244
; Patent No. 5891719
; GENERAL INFORMATION:
; APPLICANT: Cohen, Lucy
; APPLICANT: Baeuerle, Patrick
; TITLE OF INVENTION: IKAP Proteins, Nucleic Acids and Methods
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
; STREET: 75 DENISE DRIVE
; CITY: HILLSBOROUGH
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94010
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/971,244
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: OSMAN, RICHARD A
; REGISTRATION NUMBER: 36,627
; REFERENCE/DOCKET NUMBER: T97-011
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 343-4341
; TELEFAX: (650) 343-4342
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3999 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..3996
US-08-971-244-1

Query Match 97.3%; Score 14.6; DB 2; Length 3999;
Best Local Similarity 93.3%;
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GGTTCACSGATTGTC 15
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1 GGTTCACGGATTGTC 15

Db 2080 GGTTCACGGATTGTC 2094

RESULT 2
US-09-286-891-1
Sequence 1, Application US/09286891
Patent No. 6172195
GENERAL INFORMATION:
; APPLICANT: Cohen, Lucy
; APPLICANT: Baeuerle, Patrick
; TITLE OF INVENTION: IKAP Proteins, Nucleic Acids and Methods
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
; STREET: 75 DENISE DRIVE
; CITY: HILLSBOROUGH
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94010
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/286,891
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/971,244
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: OSMAN, RICHARD A
; REGISTRATION NUMBER: 36,627
; REFERENCE/DOCKET NUMBER: T97-011
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 343-4341
; TELEFAX: (650) 343-4342
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..3996
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3999 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA

Query Match   97.3%; Score 14.6; DB 3; Length 3999;
Best Local Similarity   93.3%; Pred. No. 34;
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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Db   2080 GGTTCACGGATTGTC 2094
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RESULT 3
US-09-270-767-13909
Sequence 13909, Application US/09270767
Patent No. 6703491
GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 13909
; LENGTH: 798

; TYPE: DNA
; ORGANISM: Drosophila melanogaster
US-09-270-767-13909

Query Match   90.7%; Score 13.6; DB 4; Length 798;
Best Local Similarity   92.9%; Pred. No. 1.1e+02;
Matches 13; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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Qy      2 GGTTCACSGATTGTC 15
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Db    249 GGTTCACGGATTGTC 262
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RESULT 4
US-09-270-767-28047
Sequence 28047, Application US/09270767
Patent No. 6703491
GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 28047
; LENGTH: 242
; TYPE: DNA
; ORGANISM: Drosophila melanogaster
US-09-270-767-28047

Query Match   86.7%; Score 13; DB 4; Length 242;
Best Local Similarity   86.7%; Pred. No. 2.3e+02;
Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

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Qy      1 GGTTCACSGATTGTC 15
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Db    143 GGTGCACCGATTGTC 157
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RESULT 5
US-09-270-767-12302
Sequence 12302, Application US/09270767
Patent No. 6703491
GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 12302
; LENGTH: 347
; TYPE: DNA
; ORGANISM: Drosophila melanogaster
US-09-270-767-12302

Query Match   86.7%; Score 13; DB 4; Length 347;
Best Local Similarity   86.7%; Pred. No. 2.4e+02;
Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

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Qy      1 GGTTCACSGATTGTC 15
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Db    248 GGTGCACCGATTGTC 262
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RESULT 6
US-09-252-991A-2680/c
Sequence 2680, Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.

QM nucleic - nucleic search, using sw model

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

Run on: July 31, 2005, 14:44:02 ; Search time 431.759 Seconds
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                 1683.411 Million cell updates/sec

Title: US-10-041-856-85
Perfect score: 15
Sequence: 1 aagtaagygccattg 15

Scoring table: IDENTITY_NUC
                 Gapop 10.0 , Gapext 1.0
Searched: 4708233 seqs, 2422707955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

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                 13: gb_un:*
                 14: gb_vi:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	14.6	97.3	15	6	AX676132	AX676132 Sequence
2	14.6	97.3	312	11	HSPA32D12	Z94216 H.sapiens f
3	14.6	97.3	1165	8	AK111717	AK111717 Oryza sat
4	14.6	97.3	20938	9	AY613922	AY613922 Homo sapi
5	14.6	97.3	37552	8	SC9302X	Z48179 S.cerevisia
6	14.6	97.3	6479	6	AX676048	AX676048 Sequence
7	14.6	97.3	78376	9	AL359692	AL359692 Human DNA
8	14.6	97.3	83905	2	AC025337	AC025337 Homo sapi
9	14.6	97.3	102200	9	HS30M3	AL031775 Human DNA
10	14.6	97.3	104339	2	AF235105	AF235105 Homo sapi
11	14.6	97.3	105335	9	AC107374	AC107374 Homo sapi
12	14.6	97.3	110000	8	CR882123.10	Continuation (11 o
13	14.6	97.3	11581	10	AL807245	AL807245 Mouse DNA
14	14.6	97.3	146022	5	AC026881	AC026881 Homo sapi
15	14.6	97.3	147460	5	BX255929	BX255929 Zebrafish
16	14.6	97.3	149866	9	AC025627	AC025627 Homo sapi
17	14.6	97.3	150355	9	AL359692	AL359692 Human DNA
18	14.6	97.3	150846	2	HSJ364H10	HSJ364H10 Human DN
19	14.6	97.3	152077	9	AC036173	AC036173 Homo sapi
20	14.6	97.3	152448	8	AP004339	AP004339 Oryza sat
21	14.6	97.3	154883	9	AC068711	AC068711 Homo sapi
22	14.6	97.3	159609	2	AC141905	AC141905 Rattus no
23	14.6	97.3	159908	9	AC069277	AC069277 Homo sapi
24	14.6	97.3	162778	9	AC009559	AC009559 Homo sapi
25	14.6	97.3	165049	9	AL159995	AL159995 Human DNA
26	14.6	97.3	166488	9	AC026179	AC026179 Homo sapi
27	14.6	97.3	167726	2	AC012580	AC012580 Homo sapi
28	14.6	97.3	167726	9	AC115898	AC115898 Homo sapi
29	14.6	97.3	174208	9	CNS01DVA	CNS01DVA Human chr
30	14.6	97.3	174408	2	AC015935	AC015935 Homo sapi
31	14.6	97.3	175780	2	AC138678	AC138678 Mus muscu
32	14.6	97.3	185196	2	AC023939	AC023939 Mus muscu
33	14.6	97.3	191304	5	AL928675	AL928675 Zebrafish
34	14.6	97.3	194201	2	AC148038	AC148038 Ovis arie
35	14.6	97.3	204794	9	AC024897	AC024897 Homo sapi
36	14.6	97.3	204797	9	AC024154	AC024154 Homo sapi
37	14.6	97.3	213701	10	AC125410	AC125410 Mus muscu
38	14.6	97.3	217043	2	AC026932	AC026932 Homo sapi
39	14.6	97.3	217912	9	AC094349	AC094349 Homo sapi
40	14.6	97.3	223854	9	AL606962	AL606962 Mouse DNA
41	14.6	97.3	224991	2	AC148953	AC148953 Otolemur
42	14.6	97.3	235033	6	BD084121	BD084121 Polymorph
43	14.6	97.3	236644	2	AC109122	AC109122 Rattus no
44	14.6	97.3	237226	6	BD084122	BD084122 Polymorph
45	14.6	97.3	246240	6	AR036572	AR036572 Sequence

ALIGNMENTS

RESULT 1
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LOCUS   AX676132   15 bp   DNA   linear   PAT 27-MAR-2003
DEFINITION   Sequence 85 from Patent WO02059381.
ACCESSION   AX676132
VERSION   AX676132.1 GI:29333816
KEYWORDS
SOURCE   synthetic construct
  ORGANISM   synthetic construct
             other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Slaugenhaupt,S. and Gusella,J.F.
  TITLE   Gene for identifying individuals with familial dysautonomia
  JOURNAL   Patent: WO 02059381-A 85 01-AUG-2002;
             The General Hospital Corporation (US)
FEATURES   Location/Qualifiers
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                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
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Query Match   97.3%; Score 14.6; DB 6; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.4e+03;
Matches 15; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   1 AAGTAAGYGCCATTG 15
              |||||||||||||||
Db   1 AAGTAAGYGCCATTG 15

RESULT 2
HSPA32D12/c

LOCUS   HSPA32D12   312 bp   DNA   linear   STS 21-MAY-1998
DEFINITION   H.sapiens flow-sorted chromosome 6 HindIII fragment, SC6pA32D12,
             sequence tagged site.
ACCESSION   Z94216
VERSION   Z94216.1 GI:1945210
KEYWORDS   STS; single read.
SOURCE   Homo sapiens (human)
  ORGANISM   Homo sapiens

COMMENT
FEATURES
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ORIGIN

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Best Local Similarity   93.3%;   Pred. No. 1.7e+03;
Matches 14; Conservative   1; Mismatches 0; Indels   0; Gaps   0;

Qy   1 AAGTAAGYGCCATTG 15
          ||||||:|:||||||
Db   38 AAGTAAGTGCCATTG 24

REFERENCE
  1 (bases 1 to 312)
  AUTHORS   Mungall,A.J., Huckle,E., Langford,C., Ross,M.T. and Hunt,S.E.
  TITLE   Direct Submission
  JOURNAL   Submitted (17-APR-1997) The Sanger Centre, Wellcome Trust Genome
            Campus, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail contact:
            humquery@sanger.ac.uk

COMMENT   Vector: pBS1ISK+

RESULT 3
LOCUS   AK111717
ACCESSION   AK111717/c
DEFINITION Oryza sativa (japonica cultivar-group) mRNA   linear   PLN 29-OCT-2003
            insert sequence.
VERSION   AK111717.1 GI:37988380
KEYWORDS   FLI_cDNA; CAP trapper.
SOURCE   Oryza sativa (japonica cultivar-group)
  ORGANISM Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1
  AUTHORS   The Rice Full-Length cDNA Consortium, National Institute of
            Agrobiological Sciences Rice Full-Length cDNA Project Team:,
            Kikuchi,S., Satoh,K., Nagata,T., Kawagashira,N., Doi,K.,
            Kishimoto,N., Yazaki,J., Ishikawa,M., Yamada,H., Ooka,H., Hotta,I.,
            Kojima,K., Namiki,T., Ohneda,E., Yahagi,W., Suzuki,K., Li,C., Lu,M.,
            Ohtsuki,K., Shishiki,T., Foundation of Advancement of International
            Science Genome Sequencing & Analysis Group:, Otomo,Y., Murakami,K.,
            Iida,Y., Sugano,S., Fujimura,T., Suzuki,Y., Tsunoda,Y.,
            Kurosaki,T., Kodama,T., Masuda,H., Kobayashi,M., Xie,Q., Lu,M.,
            Kurosaki,T., Kodama,T., Masuda,H., Kobayashi,M., Xie,Q., Lu,M.,
            Narikawa,R., Sugiyama,A., Mizuno,K., Yokomizo,S., Niikura,J.,
            Ikeda,R., Ishibiki,J., Kawamata,M., Yoshimura,A., Miura,J.,
            Kusunegi,T., Oka,M., Ryu,R., Ueda,M., Matsubara,K., RIKEN:,
            Kawai,J., Carninci,P., Adachi,J., Aizawa,K., Arakawa,T., Fukuda,S.,
            Hara,A., Hashidume,W., Hayatsu,N., Imotani,K., Ishii,Y., Itoh,M.,
            Kagawa,I., Kondo,S., Konno,H., Miyazaki,A., Osato,N., Ota,Y.,
            Saito,R., Sasaki,D., Sato,K., Shibata,K., Shinagawa,A., Shiraki,T.,
            Yoshino,M. and Hayashizaki,Y.,
  TITLE   Collection, mapping, and annotation of over 28,000 cDNA clones from
            japonica rice
  JOURNAL   Science 301 (5631), 376-379 (2003)
  MEDLINE   22752273
  PUBMED   12869764
REFERENCE   2
  AUTHORS   Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Carninci,P., Doi,K.,
            Fujimura,T., Fukuda,S., Hanagaki,T., Hara,A., Hashizume,W.,
            Hayashida,K., Hayashizaki,Y., Hiramoto,K., Hiraoka,T.,

REFERENCE
FEATURES
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  /mol_type="mRNA"
  /cultivar="Nipponbare"
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ORIGIN

Query Match   97.3%;   Score 14.6; DB 8;   Length 1165;
Best Local Similarity   93.3%;   Pred. No. 1.4e+03;
Matches 14; Conservative   1; Mismatches 0; Indels   0; Gaps   0;

Qy   1 AAGTAAGYGCCATTG 15
          ||||||:|:||||||
Db   61 AAGTAAGCGCCATTG 47

LOCUS   AK111717   1165 bp   mRNA   linear   PLN 29-OCT-2003
DEFINITION Oryza sativa (japonica cultivar-group) cDNA clone:J023022A01, full
COMMENT   This clone is one of the 32K full-length cDNA clones from japonica
            rice.
            URL : http://cdna01.dna.affrc.go.jp/cDNA/
            NIAS Rice Full-Length cDNA Project Team: Kikuchi,S., Satoh,K.,
            Nagata,T., Kawagashira,N., Doi,K., Kishimoto,N., Yazaki,J.,
            Ishikawa,M., Yamada,H., Ooka,H., Hotta,I., Kojima,K., Namiki,T.,
            Ohneda,E., Yahagi,W., Suzuki,K., Li,C., Ohtsuki,K., Shishiki,T.,
            Yamamoto,M. and Nakahama,Y.
            FAIS Genome Sequencing & Analysis Group: Otomo,Y., Iida,Y.,
            Fujimura,T., Ikeda,R., Ishibiki,J., Kawamata,M.,
            Kobayashi,M., Kodama,T., Kurosaki,T., Kusunegi,T., Lu,M., Oka,M.,
            Masuda,H., Miura,J., Mizuno,K., Narikawa,R., Niikura,J., Ueda,M.,
            Ryu,R., Sugano,S., Sugiyama,A., Suzuki,Y., Tsunoda,Y., Yoshimura,A.,
            Xie,Q., Yokomizo,S., Yoshimura,A. and Murakami,K.
            Genome Exploration Research Group in Rikken Genomic Sciences Center
            and Genome Science Laboratory in Rikken: Adachi,J., Aizawa,K.,
            Akimura,T., Arakawa,T., Carninci,P., Fukuda,S., Hanagaki,T.,
            Hara,A., Hashizume,W., Hayashida,K., Hayatsu,N., Hiramoto,K.,
            Hiraoka,T., Horii,F., Iida,J., Imamura,K., Imotani,K., Ishii,Y.,
            Itoh,M., Kagawa,I., Kanagawa,S., Katoh,H., Kawai,J.,
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            Nakamura,M., Nishi,K., Nomura,K., Numasaki,R., Ohno,M., Osato,N.,
            Ota,Y., Saitoh,H., Sakai,C., Sakai,Y.,
            Sakazume,N., Sano,H., Sasaki,D., Sato,K., Shibata,K.,
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            Takaku-Akahira,S., Tanaka,T., Tomaru,A., Toya,T., Waki,K.,
            Yasunishi,A. and Hayashizaki,Y.
REFERENCE   3 (bases 1 to 1165)
  AUTHORS   Kikuchi,S.
  TITLE   Rice full-length cDNA
  JOURNAL   Unpublished
REFERENCE   TITLE   Direct Submission
  JOURNAL   Submitted (12-SEP-2002) Shoshi Kikuchi, National Institute of
            Agrobiological Sciences, Department of Molecular Genetics, Head of
            Laboratory of Gene Expression; 2-1-2 Kannondai, Tsukuba, Ibaraki
            305-8602, Japan (E-mail:skikuchi@nias.affrc.go.jp,
            Tel:81-29-838-7007, Fax:81-29-838-7007)

REFERENCE
  AUTHORS   Hori,F., Hotta,I., Iida,J., Iida,Y., Ikeda,R., Imamura,K.,
            Imotani,K., Ishibiki,J., Ishii,Y., Ishikawa,M., Itoh,M., Kagawa,I.,
            Kanagawa,S., Katoh,H., Kawagashira,N., Kawai,J., Kawamata,M.,
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OM nucleic - nucleic search, using sw model

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Title: US-10-041-856-85
Perfect score: 15
Sequence: 1 aagtaagygccattg 15
Scoring table: IDENTITY NUC
                   Gapop 10.0 , Gapext 1.0
Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

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13: geneseqn2004bs:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	14.6	97.3	15	6	ABQ80561	Abq80561 IKBKAP pr
2	14.6	97.3	369	10	ADK56433	Adk56433 Plant DNA
3	14.6	97.3	593	10	ADK56971	Adk56971 Plant DNA
4	14.6	97.3	66479	6	ABQ80567	Abq80567 Mutant hu
5	14.6	97.3	66479	6	ABQ80566	Abq80566 Mutant hu
6	14.6	97.3	66479	6	ABQ80568	Abq80568 Mutant hu
7	14.6	97.3	66479	6	ABQ80565	Abq80565 Human IKB
8	14.6	97.3	237326	2	AAV57903	Aav57903 Hereditar
9	14.6	97.3	228	6	ABQ67963	Abq67963 Listeria
10	14.6	97.3	390	10	ADH83551	Adh83551 Enterococ
11	13.6	90.7	430	6	ABK30463	Abk30463 Human G-p
12	13.6	90.7	570	6	AAS96719	Aas96719 Corn DMT
13	13.6	90.7	570	11	ADM39599	Adm39599 DMT polyn
14	13.6	90.7	595	6	AAS96714	Aas96714 Corn DMT
15	13.6	90.7	595	11	ADM39589	Adm39589 DMT polyn
16	13.6	90.7	751	10	ADK60125	Adk60125 Plant DNA
17	13.6	90.7	1020	2	AAT40142	Aat40142 A. niger
18	13.6	90.7	1446	6	ABZ78269	Abz78269 A. niger
19	13.6	90.7	1453	2	AAX13183	Aax13183 Enterococ
20	13.6	90.7	1453	6	ABS98978	Abs98978 Enterococ
c 21	13.6	90.7	1587	13	ADR88965	Adr88965 A. thalia
c 22	13.6	90.7	1957	4	ABA46165	Aba46165 Human bre
c 23	13.6	90.7	1957	4	AAK30368	Aak30368 Human bon
c 24	13.6	90.7	2360	2	AAT40148	Aat40148 A. niger
c 25	13.6	90.7	2520	6	ABZ78212	Abz78212 A. niger
c 26	13.6	90.7	3105	10	ADF03715	Adf03715 Bacterial
c 27	13.6	90.7	3172	13	ADS10043	Ads10043 Human the
c 28	13.6	90.7	3774	4	AAK70878	Aak70878 Human imm
c 29	13.6	90.7	6242	6	ABQ70961	Abq70961 Listeria
c 30	13.6	90.7	7355	12	ADN49781	Adn49781 Turkey as
c 31	13.6	90.7	12462	4	ABL05490	Abl05490 Drosophil
c 32	13.6	90.7	12481	4	ABL20544	Abl20544 Partial s
c 33	13.6	90.7	13417	2	AAT09224	Aat09224 Pseudomon
c 34	13.6	90.7	26705	12	ADQ62810	Adq62810 Pseudomon
c 35	13.6	90.7	32986	4	AAK69758	Aak69758 Human imm
c 36	13.6	90.7	33986	6	AAK84629	Aak84629 Human imm
c 37	13.6	90.7	50000	2	AAX23517	Aax23517 Human kid
c 38	13.6	90.7	56258	11	ACN44456	Acn44456 Mouse gen
c 39	13.6	90.7	62488	6	AAD44981	Aad44981 Human EMR
c 40	13.6	90.7	110000	6	ABQ59245_14	Abq59245_14
c 41	13.6	90.7	110000	6	ABQ67195_3	Abq67195_3
c 42	13.6	90.7	110000	6	ABA03041_14	Aba03041_14
c 43	13.6	90.7	151152	13	ADR52892	Adr52892 Drug ther
c 44	13.6	90.7	163382	13	ABD32659	Abd32659 Human can
c 45	13.6	90.7	349980	6	ABQ81845	Abq81845 Bifidobac

ALIGNMENTS

RESULT 1
ABQ80561

ID   ABQ80561 standard; DNA; 15 BP.
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AC   ABQ80561;
XX
DT   08-NOV-2002 (first entry)
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DE   IKBKAP probe #1.
XX
KW   Human; IKBKAP; Familial Dysautonomia; FD; Riley-Day syndrome;
KW   Hereditary Sensory and Autonomic Neuropathy Type III; carrier screening;
KW   probe; ss.
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OS   Homo sapiens.
XX
PN   WO200259381-A2.
XX
PD   01-AUG-2002.
XX
PF   07-JAN-2002; 2002WO-US000473.
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PR   06-JAN-2001; 2001US-0260080P.
XX
PA   (GEHO) GEN HOSPITAL CORP.
XX
PI   Slaugenhaupt S, Gusella JF;
XX
DR   WPI; 2002-674806/72.
XX
PT   New IKBKAP genes with mutations, useful for identifying a subject with
PT   familial dysautonomia (FD), or for rapid carrier screening in the
PT   Ashkenazi Jewish population, e.g. screening presymptomatic homozygotes or
PT   prenatal diagnosis.
XX
PS   Claim 27; Page 43; 109pp; English.
XX
CC   The present invention relates to methods and compositions useful for
CC   detecting mutations which cause Familial Dysautonomia (FD, Riley-Day
CC   syndrome, Hereditary Sensory and Autonomic Neuropathy Type III) (OMIM
CC   223900). It was found that mutations in the IKBKAP gene (see ABQ80565)
CC   are associated with FD. The mutation associated with the major haplotype
CC   of FD, FD1 mutation, is a base pair (bp) mutation, where the thymine

Left column

```
CC   nucleotide located at bp 6 of intron 20 in the IKBKAP gene is replaced
CC   with a cytosine. This results in skipping of exon 20 in the mRNA from FD
CC   patients, although they continue to express varying levels of wild-type
CC   message in a tissue-specific manner. The mutation associated with the
CC   minor haplotype, FD2 mutation, is a bp mutation, where the guanine
CC   nucleotide at bp 2397 (bp 73 of exon 19) is replaced with a cytosine.
CC   This bp mutation causes an arginine to proline missense mutation (R696P)
CC   in the IKBKAP protein, which is predicted to disrupt a potential
CC   phosphorylation site. The IKBKAP nucleic acid sequences are useful for
CC   identifying a subject with FD and for rapid carrier screening. The IKBKAP
CC   gene maps to chromosome 9q31. Probes ABQ80561-ABQ80562 were used to
CC   detect the mutations in the IKBKAP gene
XX
SQ   Sequence 15 BP; 5 A; 2 C; 4 G; 3 T; 0 U; 1 Other;

Qy          1 AAGTAAGYGCCATTG 15
              |||||||||||||||
Db          1 AAGTAAGYGCCATTG 15

  Query Match             97.3%;  Score 14.6;  DB 6;  Length 15;
  Best Local Similarity   100.0%;             Pred. No. 1e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

RESULT 2
ADK56433/c
ID   ADK56433 standard; DNA; 369 BP.
XX
AC   ADK56433;
XX
DT   06-MAY-2004  (first entry)
XX
DE   Plant DNA sequence which confers altered metabolic characteristic #3816.
XX
KW   altered metabolic characteristic; plant; acid metabolism;
KW   alcohol metabolism; fatty acid metabolism;
KW   branched fatty acid metabolism; alkaloid metabolism;
KW   amino acid metabolism; ester metabolism; glyceride metabolism;
KW   phenolic metabolism; carbohydrate metabolism; sterol metabolism;
KW   terpene metabolism; isoprenoid metabolism; alkene metabolism;
KW   alkyne metabolism; hydrocarbon metabolism; ketone metabolism;
KW   quinone metabolism; disease resistance; gene shuffling; sexual PCR; ds.
XX
OS   Hypocrea lixii.
XX
PN   WO2003020936-A1.
XX
PD   13-MAR-2003.
XX
PF   30-AUG-2002; 2002WO-US027884.
XX
PR   31-AUG-2001; 2001US-0316471P.
XX
PA   (DOWC ) DOW CHEM CO.
PA   (DOWC ) DOW AGROSCIENCES LLC.
XX
PI   Weglarz T, Gachotte D, Blakeslee B, Mccreary DA, Pell RJ;
PI   Oriedo JVB, Crosley R, Reddy AS, Shukla V, Larrinua I, Miller BA;
XX
DR   WPI; 2003-313091/30.
XX
PT   Novel genes that confer altered metabolic characteristics in Nicotiana
PT   benthamiana plants, useful for altering the levels of metabolites e.g.
PT   acids, fatty acids, amino acids, carbohydrates, hydrocarbons and sterols.
XX
PS   Claim 1; SEQ ID NO 3816; 2576pp; English.
XX
CC   The invention comprises DNA sequences which confer an altered metabolic
CC   characteristic when they are expressed in a plant. The DNA sequences of
CC   the invention are useful for producing plants with an altered metabolic
CC   characteristic, such as: altered acid metabolism, alcohol metabolism,
CC   fatty acid metabolism, branched fatty acid metabolism, alkaloid
CC   metabolism, altered amino acid metabolism, altered ester metabolism,
CC   altered glyceride metabolism, altered phenolic metabolism, altered
CC   carbohydrate metabolism, altered sterol, oxygenated terpene, or
CC   isoprenoid metabolism, alkene or alkyne metabolism, hydrocarbon
CC   metabolism, ketone or quinone metabolism. The DNA sequences of the
CC   invention may be used to provide disease resistance in a plant and gene
CC   base metabolism, altered amino acid metabolism, altered ester metabolism,
```

Right column

```
Qy          1 AAGTAAGYGCCATTG 15
              ||||||||:||||||
Db         43 AAGTAAGCGCCATTG 29

  Query Match             97.3%;  Score 14.6;  DB 10;  Length 369;
  Best Local Similarity   93.3%;              Pred. No. 1.5e+02;
  Matches   14;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

SQ   Sequence 369 BP; 125 A; 70 C; 75 G; 99 T; 0 U; 0 Other;

CC   altered glyceride metabolism, altered phenolic metabolism, altered
CC   carbohydrate metabolism, altered sterol, oxygenated terpene, or
CC   isoprenoid metabolism, alkene or alkyne metabolism, hydrocarbon
CC   metabolism, ketone or quinone metabolism. The DNA sequences of the
CC   invention may be used to provide disease resistance in a plant and gene
CC   shuffling or sexual PCR procedures. The present nucleic acid represents a
CC   DNA sequence of the invention.

RESULT 3
ADK56971/c
ID   ADK56971 standard; DNA; 593 BP.
XX
AC   ADK56971;
XX
DT   06-MAY-2004  (first entry)
XX
DE   Plant DNA sequence which confers altered metabolic characteristic #4354.
XX
KW   altered metabolic characteristic; plant; acid metabolism;
KW   alcohol metabolism; fatty acid metabolism;
KW   branched fatty acid metabolism; alkaloid metabolism;
KW   amino acid metabolism; ester metabolism; glyceride metabolism;
KW   phenolic metabolism; carbohydrate metabolism; sterol metabolism;
KW   terpene metabolism; isoprenoid metabolism; alkene metabolism;
KW   alkyne metabolism; hydrocarbon metabolism; ketone metabolism;
KW   quinone metabolism; disease resistance; gene shuffling; sexual PCR; ds.
XX
OS   Unidentified.
XX
PN   WO2003020936-A1.
XX
PD   13-MAR-2003.
XX
PF   30-AUG-2002; 2002WO-US027884.
XX
PR   31-AUG-2001; 2001US-0316471P.
XX
PA   (DOWC ) DOW CHEM CO.
PA   (DOWC ) DOW AGROSCIENCES LLC.
XX
PI   Weglarz T, Gachotte D, Blakeslee B, Mccreary DA, Pell RJ;
PI   Oriedo JVB, Crosley R, Reddy AS, Shukla V, Larrinua I, Miller BA;
XX
DR   WPI; 2003-313091/30.
XX
PT   Novel genes that confer altered metabolic characteristics in Nicotiana
PT   benthamiana plants, useful for altering the levels of metabolites e.g.
PT   acids, fatty acids, amino acids, carbohydrates, hydrocarbons and sterols.
XX
PS   Claim 1; SEQ ID NO 4354; 2576pp; English.
XX
CC   The invention comprises DNA sequences which confer an altered metabolic
CC   characteristic when they are expressed in a plant. The DNA sequences of
CC   the invention are useful for producing plants with an altered metabolic
CC   characteristic, such as: altered acid metabolism, alcohol metabolism,
CC   fatty acid metabolism, branched fatty acid metabolism, alkaloid
CC   base metabolism, altered amino acid metabolism, altered ester metabolism,
CC   altered glyceride metabolism, altered phenolic metabolism, altered
CC   carbohydrate metabolism, altered sterol, oxygenated terpene, or
CC   isoprenoid metabolism, alkene or alkyne metabolism, hydrocarbon
CC   metabolism, ketone or quinone metabolism. The DNA sequences of the
CC   invention may be used to provide disease resistance in a plant and gene
```

OM nucleic - nucleic search, using sw model

GenCore version 5.1.6
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Run on: July 31, 2005, 09:42:59 ; Search time 106.204 Seconds
(without alignments)
836.092 Million cell updates/sec

Title: US-10-041-856-86
Perfect score: 15
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Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0
Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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9: geneseqn2003as:*
10: geneseqn2003bs:*
11: geneseqn2003cs:*
12: geneseqn2003ds:*
11: geneseqn2004as:*
13: geneseqn2004bs:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	14.6	97.3	15	6	Abq80562	Abq80562 IKBKAP pr
2	14.6	97.3	803	4	Aah05318	Aah05318 Human cDN
3	14.6	97.3	2471	4	Aah15795	Aah15795 Human cDN
4	14.6	97.3	3999	2	Aax28025	Aax28025 Human IKA
5	14.6	97.3	3999	4	Aaf29756	Aaf29756 Human IKA
6	14.6	97.3	4417	13	Adr07102	Adr07102 Full leng
7	14.6	97.3	4788	4	Aah14533	Aah14533 Human cDN
8	14.6	97.3	4803	5	Aah81767	Aah81767 Human dif
9	14.6	97.3	4803	6	Aal44190	Aal44190 Human I-k
10	14.6	97.3	5924	6	Abq80570	Abq80570 Mutant hu
11	14.6	97.3	5924	6	Abq80569	Abq80569 Mutant IKB
12	14.6	97.3	5924	8	Acd13384	Acd13384 Human DNA
13	14.6	97.3	6479	6	Abq80567	Abq80567 Mutant hu
14	14.6	97.3	6479	6	Abq80566	Abq80566 Mutant hu
15	14.6	97.3	6479	6	Abq80568	Abq80568 Mutant hu
16	14.6	97.3	6479	6	Abq80565	Abq80565 Human IKB
17	13.6	90.7	1329	10	Acf67648	Acf67648 Photorhab
18	13.6	90.7	1920	10	Acf69565	Acf69565 Photorhab
19	13.6	90.7	3770	4	Abl15715	Abl15715 Drosophil
20	13.6	90.7	10360	4	Abl15714	Abl15714 Drosophil

c	21	13.6	90.7	110000	10	Acf65383_1	Continuation (2 of
c	22	13.6	90.7	110000	10	Acf67367_02	Continuation (3 of
c	23	13.6	90.7	110000	10	Acf67367_25	Continuation (26 o
c	24	13.6	90.7	110000	10	Acf65386_3	Continuation (4 of
c	25	13.6	86.7	330	13	Ads14489	Ads14489 Pseudomon
c	26	86.7		369	8	Abx50965	Abx50965 Bovine ES
c	27	86.7		402	6	Abq67491	Abq67491 Listeria
c	28	86.7		420	12	Adn74668	Adn74668 Thale cre
c	29	86.7		540	8	Aca20442	Aca20442 Prokaryot
c	30	86.7		546	6	Abk75286	Abk75286 Bacillus
c	31	86.7		564	10	Abx57020	Abx57020 Arabidops
c	32	86.7		639	12	Adj44170	Adj44170 Plant cDN
c	33	86.7		643	3	Aaf11156	Aaf11156 Fusarium
c	34	86.7		664	8	Aac45317	Aac45317 Arabidops
c	35	86.7		675	3	Aac36085	Aac36085 Arabidops
c	36	86.7		675	11	Abd04076	Abd04076 Pseudomon
c	37	86.7		708	3	Aac49221	Aac49221 Arabidops
c	38	86.7		710	3	Aac37069	Aac37069 Arabidops
c	39	86.7		771	8	Aca52899	Aca52899 Prokaryot
c	40	86.7		771	6	Aah67085	Aah67085 C glutami
c	41	86.7		900	4	Aaf71456	Aaf71456 Corynebac
c	42	86.7		951	10	Adc23958	Adc23958 DNA seque
c	43	86.7		951	12	Adh36059	Adh36059 Chemical
c	44	86.7		951	12	Adg93760	Adg93760 Nitrilase
c	45	86.7		951	12	Adi62357	Adi62357 DNA encod

ALIGNMENTS

RESULT 1
ABQ80562

ID ABQ80562 standard; DNA; 15 BP.
XX
AC ABQ80562;
XX
DT 08-NOV-2002 (first entry)
XX
DE IKBKAP probe #2.
XX
KW Human; IKBKAP; Familial Dysautonomia; FD; Riley-Day syndrome;
KW Hereditary Sensory and Autonomic Neuropathy Type III; carrier screening;
KW probe; ss.
XX
OS Homo sapiens.
XX
PN WO20020259381-A2.
XX
PD 01-AUG-2002.
XX
PF 07-JAN-2002; 2002WO-US000473.
XX
PR 06-JAN-2001; 2001US-0260080P.
XX
PA (GEHO) GEN HOSPITAL CORP.
XX
PI Slaugenhaupt S, Gusella JF;
XX
DR WPI; 2002-674806/72.
XX
PT New IKBKAP genes with mutations, useful for identifying a subject with
PT familial dysautonomia (FD), or for rapid carrier screening in the
PT Ashkenazi Jewish population, e.g. screening presymptomatic homozygotes or
PT prenatal diagnosis.
XX
PS Claim 27; Page 43; 109pp; English.
XX
CC The present invention relates to methods and compositions useful for
CC detecting mutations which cause Familial Dysautonomia (FD, Riley-Day
CC syndrome, Hereditary Sensory and Autonomic Neuropathy Type III) [OMIM
CC 223900]. It was found that mutations in the IKBKAP gene (see ABQ80565)
CC are associated with FD. The mutation associated with the major haplotype
CC of FD, FD1 mutation, is a base pair (bp) mutation, where the thymine

CC nucleotide located at bp 6 of intron 20 in the IKBKAP gene is replaced
CC with a cytosine. This results in skipping of exon 20 in the mRNA from FD
CC patients, although they continue to express varying levels of wild-type
CC message in a tissue-specific manner. The mutation associated with the
CC minor haplotype, FD2 mutation, is a bp mutation, where the
CC nucleotide at bp 2397 (bp 73 of exon 19) is replaced with a cytosine.
CC This bp mutation causes an arginine to proline missense mutation (R696P)
CC in the IKBKAP protein, which is predicted to disrupt a potential
CC phosphorylation site. The IKBKAP nucleic acid sequences are useful for
CC identifying a subject with FD and for rapid carrier screening. The IKBKAP
CC gene maps to chromosome 9q31. Probes ABQ80561-ABQ80562 were used to
CC detect the mutations in the IKBKAP gene
XX
SQ Sequence 15 BP; 2 A; 3 C; 4 G; 5 T; 0 U; 1 Other;
XX

Best Match
Query Match 97.3%; Score 14.6; DB 6; Length 15;
Best Local Similarity 100.0%; Pred. No. 79; Mismatches 0; Indels 0; Gaps 0;
Matches 15; Conservative 0;

Qy 1 GGTTCACSGATTGTC 15
     |||||||||||||||
Db 1 GGTTCACSGATTGTC 15

RESULT 2
ID AAH05318
   AAH05318 standard; cDNA; 803 BP.
XX
AC AAH05318;
XX
DT 26-JUN-2001 (first entry)
XX
DE Human cDNA clone (5'-primer) SEQ ID NO:2153.
XX
KW Human; primer; detection; diagnosis; antisense therapy; gene therapy; ss.
XX
OS Homo sapiens.
XX
PN EP1074617-A2.
XX
PD 07-FEB-2001.
XX
PF 28-JUL-2000; 2000EP-00116126.
XX
PR 29-JUL-1999; 99JP-00248036.
PR 27-AUG-1999; 99JP-00300253.
PR 11-JAN-2000; 2000JP-00018776.
PR 02-MAY-2000; 2000JP-00183767.
PR 09-JUN-2000; 2000JP-00241899.
XX
(HELI-) HELIX RES INST.
XX
PI Ota T, Isogai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J;
PI Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T;
XX
DR WPI; 2001-318749/34.
XX
PT Primer sets for synthesizing polynucleotides, particularly the 5602 full-
PT length cDNAs defined in the specification, and for the detection and/or
PT diagnosis of the abnormality of the proteins encoded by the full-length
PT cDNAs.
XX
PS Claim 1; SEQ ID NO 2153; 2537pp + Sequence Listing; English.
XX
CC The present invention describes primer sets for synthesizing 5602 full-
CC length cDNAs defined in the specification. Where a primer set comprises:
CC (a) an oligo-dT primer and an oligonucleotide complementary to the
CC complementary strand of a polynucleotide which comprises one of the 5602
CC nucleotide sequences defined in the specification, where the
CC oligonucleotide comprises at least 15 nucleotides; or (b) a combination
CC of an oligonucleotide comprising a sequence complementary to the
CC complementary strand of a polynucleotide which comprises a 5'-end
CC sequence and an oligonucleotide comprising a sequence complementary to a

CC polynucleotide which comprises a 3'-end sequence, where the
CC oligonucleotide comprises at least 15 nucleotides and the combination of
CC the 5'-end sequence/3'-end sequence is selected from those defined in the
CC specification. The primer sets can be used in antisense therapy and in
CC gene therapy. The primers are useful for synthesizing polynucleotides,
CC particularly full-length cDNAs. The primers are also useful for the
CC detection and/or diagnosis of the abnormality of the proteins encoded by
CC the full-length cDNAs. The primers allow obtaining of the full-length
CC cDNAs easily without any specialised methods. AAH03166 to AAH13628 and
CC AAH13633 to AAH18742 represent human cDNA sequences; AAB92446 to AAB95893
CC represent human amino acid sequences; and AAH13629 to AAH13632 represent
CC oligonucleotides, all of which are used in the exemplification of the
CC present invention
XX
SQ Sequence 803 BP; 251 A; 154 C; 172 G; 222 T; 0 U; 4 Other;
XX

Query Match 97.3%; Score 14.6; DB 4; Length 803;
Best Local Similarity 93.3%; Pred. No. 1.1e+02; Mismatches 0; Indels 0; Gaps 0;
Matches 14; Conservative 1;

Qy 1 GGTTCACSGATTGTC 15
     ||||||| |||||||
Db 72 GGTTCACGGATTGTC 86

RESULT 3
ID AAH15795
   AAH15795 standard; cDNA; 2471 BP.
XX
AC AAH15795;
XX
DT 26-JUN-2001 (first entry)
XX
DE Human cDNA sequence SEQ ID NO:14253.
XX
KW Human; primer; detection; diagnosis; antisense therapy; gene therapy; ss.
XX
OS Homo sapiens.
XX
PN EP1074617-A2.
XX
PD 07-FEB-2001.
XX
PF 28-JUL-2000; 2000EP-00116126.
XX
PR 29-JUL-1999; 99JP-00248036.
PR 27-AUG-1999; 99JP-00300253.
PR 11-JAN-2000; 2000JP-00018776.
PR 02-MAY-2000; 2000JP-00183767.
PR 09-JUN-2000; 2000JP-00241899.
XX
(HELI-) HELIX RES INST.
XX
PI Ota T, Isogai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J;
PI Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T;
XX
DR WPI; 2001-318749/34.
XX
PT Primer sets for synthesizing polynucleotides, particularly the 5602 full-
PT length cDNAs defined in the specification, and for the detection and/or
PT diagnosis of the abnormality of the proteins encoded by the full-length
PT cDNAs.
XX
PS Claim 8; SEQ ID NO 14253; 2537pp + Sequence Listing; English.
XX
CC The present invention describes primer sets for synthesizing 5602 full-
CC length cDNAs defined in the specification. Where a primer set comprises:
CC (a) an oligo-dT primer and an oligonucleotide complementary to the
CC complementary strand of a polynucleotide which comprises one of the 5602
CC nucleotide sequences defined in the specification, where the
CC oligonucleotide comprises at least 15 nucleotides; or (b) a combination
CC of an oligonucleotide comprising a sequence complementary to the
CC complementary strand of a polynucleotide which comprises a sequence
CC complementary to a

OM nucleic - nucleic search, using sw model

GenCore version 5.1.6
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Run on: July 31, 2005, 16:38:33 ; Search time 153.148 Seconds
                  (without alignments)
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Title: US-10-041-856-86
Perfect score: 15
Sequence: 1 ggttcacsgattgtc 15
Scoring table: IDENTITY NUC
                  Gapop 10.0 , Gapext 1.0
Searched: 7287783 seqs, 3236178273 residues

Total number of hits satisfying chosen parameters: 14575566

Post-processing: Minimum Match 0%
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SUMMARIES

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

Result No.	Score	% Query Match	Length	DB	ID	Description
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3	14.6	97.3	201	20	US-10-719-993-4527	Sequence 4527, Ap
4	14.6	97.3	201	20	US-10-719-993-4556	Sequence 4556, Ap
5	14.6	97.3	201	20	US-10-719-993-4585	Sequence 4585, Ap
6	14.6	97.3	201	20	US-10-719-993-4613	Sequence 4613, Ap
7	14.6	97.3	201	20	US-10-719-993-34995	Sequence 34995, A
8	14.6	97.3	4256	20	US-10-719-993-319	Sequence 319, App
9	14.6	97.3	4803	10	US-09-930-213-276	Sequence 276, App
10	14.6	97.3	4803	21	US-10-956-157-1094	Sequence 1094, Ap
11	14.6	97.3	5840	20	US-10-719-993-322	Sequence 322, App
12	14.6	97.3	5924	13	US-10-041-856-2	Sequence 2, Appli
13	14.6	97.3	5957	20	US-10-719-993-320	Sequence 320, App
14	14.6	97.3	6107	20	US-10-719-993-321	Sequence 321, App
15	14.6	97.3	6179	20	US-10-719-993-318	Sequence 318, App
16	14.6	97.3	6479	13	US-10-041-856-1	Sequence 1, Appli
17	14.3	89.3	78978	20	US-10-719-993-6863	Sequence 6863, Ap
18	13.4	89.3	2365	21	US-10-719-900-625520	Sequence 622520,
19	13.4	89.3	25	18	US-10-424-599-141749	Sequence 141749,
20	13	86.7	25	21	US-10-719-900-2420	Sequence 2420, Ap
21	13	86.7	25	22	US-10-719-900-718633	Sequence 718633,
22	13	86.7	25	22	US-10-719-956-459049	Sequence 459049,
23	13	86.7	25	22	US-10-719-956-534331	Sequence 534331,
24	13	86.7	253	18	US-10-424-599-67860	Sequence 67860, A
25	13	86.7	330	18	US-10-389-647-44	Sequence 44, Appl
26	13	86.7	369	9	US-09-983-965-894	Sequence 894, App
27	13	86.7	386	20	US-10-425-115-102611	Sequence 102611,
28	13	86.7	402	17	US-10-398-221-304	Sequence 304, App
29	13	86.7	408	13	US-10-027-632-44467	Sequence 44467, A
30	13	86.7	408	17	US-10-027-632-66788	Sequence 66788, A
31	13	86.7	409	13	US-10-027-632-67332	Sequence 67332, A
32	13	86.7	409	13	US-10-027-632-311246	Sequence 311246,
33	13	86.7	409	13	US-10-027-632-311246	Sequence 311246,
34	13	86.7	409	13	US-10-027-632-311247	Sequence 311247,
35	13	86.7	409	13	US-10-027-632-66788	Sequence 66788, A
36	13	86.7	409	17	US-10-027-632-67332	Sequence 67332, A
37	13	86.7	409	13	US-10-027-633-311246	Sequence 311246,
38	13	86.7	414	13	US-10-027-633-311247	Sequence 311247,
39	13	86.7	414	20	US-10-425-115-122345	Sequence 122345,
40	13	86.7	524	20	US-10-425-115-173809	Sequence 173809,
41	13	86.7	533	18	US-10-425-114-35913	Sequence 35913, A
42	13	86.7	540	17	US-10-282-122A-8312	Sequence 8312, Ap
43	13	86.7	546	9	US-09-974-300-2577	Sequence 2577, Ap
44	13	86.7	564	9	US-09-770-152-372	Sequence 372, App
45	13	86.7	624	13	US-09-027-632-245629	Sequence 245629,

ALIGNMENTS

RESULT 1
US-10-041-856-86
; Sequence 86, Application US/10041856
; Publication No. US20020169299A1
; GENERAL INFORMATION:
; APPLICANT: SLAUGENHAUPT, SUSAN
; APPLICANT: GUSELLA, JAMES F.
; TITLE OF INVENTION: GENE FOR IDENTIFYING INDIVIDUALS WITH FAMILIAL
; TITLE OF INVENTION: DYSAUTONOMIA
; FILE REFERENCE: 1829-4004US1
; CURRENT APPLICATION NUMBER: US/10/041,856
; CURRENT FILING DATE: 2002-07-08
; PRIOR APPLICATION NUMBER: 60/260,080
; PRIOR FILING DATE: 2001-01-06
; NUMBER OF SEQ ID NOS: 88
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 86
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Probe
US-10-041-856-86

Query Match   97.3%; Score 14.6; DB 13; Length 15;
Best Local Similarity   100.0%; Pred. No. 1.4e+02;
Matches   15; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   1 GGTTCACSGATTGTC 15
              |||||||||||||||

Db   1 GGTTCACSGATTGTC 15

RESULT 2
US-10-719-993-4499
; Sequence 4499, Application US/10719993
; Publication No. US20040265849A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: ALZHEIMER'S DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001496
; CURRENT APPLICATION NUMBER: US/10/719,993
; CURRENT FILING DATE: 2003-11-24
; NUMBER OF SEQ ID NOS: 55342
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 4499
; LENGTH: 201
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-719-993-4499

  Query Match   97.3%; Score 14.6; DB 20; Length 201;
  Best Local Similarity   100.0%; Pred. No. 1.7e+02;
  Matches   15; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   1 GGTTCACSGATTGTC 15
              |||||||||||||||
Db   94 GGTTCACSGATTGTC 108

RESULT 3
US-10-719-993-4527
; Sequence 4527, Application US/10719993
; Publication No. US20040265849A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: ALZHEIMER'S DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001496
; CURRENT APPLICATION NUMBER: US/10/719,993
; CURRENT FILING DATE: 2003-11-24
; NUMBER OF SEQ ID NOS: 55342
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 4527
; LENGTH: 201
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-719-993-4527

  Query Match   97.3%; Score 14.6; DB 20; Length 201;
  Best Local Similarity   100.0%; Pred. No. 1.7e+02;
  Matches   15; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   1 GGTTCACSGATTGTC 15
              |||||||||||||||
Db   94 GGTTCACSGATTGTC 108

RESULT 4
US-10-719-993-4556
; Sequence 4556, Application US/10719993
; Publication No. US20040265849A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: ALZHEIMER'S DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001496
; CURRENT APPLICATION NUMBER: US/10/719,993
; CURRENT FILING DATE: 2003-11-24
; NUMBER OF SEQ ID NOS: 55342
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 4556
; LENGTH: 201
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-719-993-4556

  Query Match   97.3%; Score 14.6; DB 20; Length 201;
  Best Local Similarity   100.0%; Pred. No. 1.7e+02;
  Matches   15; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   1 GGTTCACSGATTGTC 15
              |||||||||||||||
Db   94 GGTTCACSGATTGTC 108

RESULT 5
US-10-719-993-4585
; Sequence 4585, Application US/10719993
; Publication No. US20040265849A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: ALZHEIMER'S DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001496
; CURRENT APPLICATION NUMBER: US/10/719,993
; CURRENT FILING DATE: 2003-11-24
; NUMBER OF SEQ ID NOS: 55342
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 4585
; LENGTH: 201
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-719-993-4585

  Query Match   97.3%; Score 14.6; DB 20; Length 201;
  Best Local Similarity   100.0%; Pred. No. 1.7e+02;
  Matches   15; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   1 GGTTCACSGATTGTC 15
              |||||||||||||||
Db   94 GGTTCACSGATTGTC 108

RESULT 6
US-10-719-993-4613
; Sequence 4613, Application US/10719993
; Publication No. US20040265849A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: ALZHEIMER'S DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001496
; CURRENT APPLICATION NUMBER: US/10/719,993
; CURRENT FILING DATE: 2003-11-24
; NUMBER OF SEQ ID NOS: 55342
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 4613
; LENGTH: 201
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-719-993-4613

  Query Match   97.3%; Score 14.6; DB 20; Length 201;
  Best Local Similarity   100.0%; Pred. No. 1.7e+02;
  Matches   15; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   1 GGTTCACSGATTGTC 15
              |||||||||||||||
Db   94 GGTTCACSGATTGTC 108

RESULT 7
US-10-719-993-34995
; Sequence 34995, Application US/10719993

OM nucleic - nucleic search, using sw model

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GenCore version 5.1.6

Run on: July 31, 2005, 15:46:58 ; Search time 734.537 Seconds
                                       (without alignments)
                                       777.311 Million cell updates/sec

Title: US-10-041-856-86
Perfect score: 15
Sequence: 1 ggttcacsgattgtc 15
Scoring table: IDENTITY_NUC
              Gapop 10.0 , Gapext 1.0
Searched: 34239544 seqs, 19032134700 residues
Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   EST:*
              1: gb_est1:*
              2: gb_est2:*
              3: gb_htc:*
              4: gb_est3:*
              5: gb_est4:*
              6: gb_est5:*
              7: gb_est6:*
              8: gb_gss1:*
              9: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	Query Match	Length	DB	ID	Description
	1	14.6	97.3	417	7	CN256146	CN256146 170005321
	2	14.6	97.3	447	2	BF840993	BF840993 RC3-HT097
c	3	14.6	97.3	513	1	AL702133	AL702133 DKFZp686G
c	4	14.6	97.3	524	4	BI647985	BI647985 603276059
c	5	14.6	97.3	553	4	BM512007	BM512007 ij77dil.x
	6	14.6	97.3	567	7	CO794653	CO794653 NT144A.H1
	7	14.6	97.3	580	5	BP243833	BP243833
	8	14.6	97.3	603	5	BX478139	BX478139 DKFZp686B
	9	14.6	97.3	618	4	BG395601	BG395601 602458222
	10	14.6	97.3	641	5	BQ807986	BQ807986 NISC_kk12
	11	14.6	97.3	686	8	BH985208	BH985208 oe169d05.
	12	14.6	97.3	694	5	BP152797	BP152797
	13	14.6	97.3	709	7	CN256149	CN256149 17000424
c	14	14.6	97.3	777	8	BH944352	BH944352 obu89b12.
	15	14.6	97.3	803	1	AU124100	AU124100
	16	14.6	97.3	866	5	BU508979	BU508979
	17	14.6	97.3	874	5	BU156074	BU156074 AGENCOURT
	18	14.6	97.3	911	2	BE256729	BE256729
	19	14.6	97.3	931	8	BG286503	BG286503 602382995
	20	14.6	97.3	982	8	B2786955	B2786955 PUGBB42TB
	21	14.6	97.3	1134	7	CN641971	CN641971 ILLUMIGEN
	22	14.6	97.3	3833	7	CR749385	CR749385 Homo sapi
	23	14.6	97.3	3999	9	AY414501	AY414501 Homo sapi
	24	14.6	97.3	3999	9	AY414502	AY414502 Pan trogl
	25	13.6	90.7	247	1	AA260845	AA260845 val9c12.r
	26	13.6	90.7	258	6	CA609548	CA609548 wr1.pk010
	27	13.6	90.7	260	8	AQ073317	AQ073317 1(3)03719
	28	13.6	90.7	269	1	AI896149	AI896149 EST265992
	29	13.6	90.7	295	9	CC848090	CC848090 NDL.117P1
	30	13.6	90.7	300	7	CO278011	CO278011 EK128503.
	31	13.6	90.7	311	2	AW031051	AW031051 EST274358
	32	13.6	90.7	321	6	CA639543	CA639543 wrein.pko
	33	13.6	90.7	323	6	CA649351	CA649351 wrein.pk0
	34	13.6	90.7	338	2	CA652678	CA652678 wrein.pk1
	35	13.6	90.7	340	6	CA612274	CA612274 wr1.pk013
	36	13.6	90.7	368	3	CNS08VRT	CNS08VRT Single re
	37	13.6	90.7	373	4	BG141075	BG141075 EST481517
	38	13.6	90.7	381	2	AW217022	AW217022 EST295736
	39	13.6	90.7	401	4	BI422386	BI422386 EST533052
c	40	13.6	90.7	401	8	BY601592	BY601592 BY601592
c	41	13.6	90.7	427	8	BH818839	BH818839 BACPP11-J
c	42	13.6	90.7	436	6	CA640314	CA640314 wrein.pko
	43	13.6	90.7	445	1	AI895520	AI895520 EST264963
	44	13.6	90.7	449	1	AI293974	AI293974 LP07249.5
	45	13.6	90.7	458	2	AW344428	AW344428 24644 MAR

ALIGNMENTS

RESULT 1
CN256146

LOCUS   CN256146   417 bp   mRNA   linear   EST 16-MAY-2004
DEFINITION 1700053218935 GRN_ES Homo sapiens cDNA 5', mRNA sequence.
ACCESSION   CN256146
VERSION   CN256146.1 GI:47272560
KEYWORDS   EST.
SOURCE   Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 417)
AUTHORS   Brandenberger,R., Wei,H., Zhang,S., Lei,S., Murage,J., Fisk,G.J.,
            Li,Y., Xu,C., Fang,R., Guegler,K., Rao,M.S., Mandalam,R.,
            Lebkowski,J and Stanton,L.W.
TITLE   Transcriptome characterization elucidates signaling networks that
            control human ES cell growth and differentiation
JOURNAL   Nat. Biotechnol. 22 (6), 707-716 (2004)
COMMENT   Contact: Brandenberger R
            Regenerative Medicine
            Geron Corporation
            230 Constitution Drive, Menlo Park, CA 94025, USA
            Tel: 650 473 8658
            Fax: 650 473 7760
            Email: rbrandenberger@geron.com
            Insert Length: 417   Std Error: 0.00.
FEATURES   Location/Qualifiers
     source   1..417
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /tissue_type="embryonic stem cells, cell lines H1, H7, and
                     H9"
                     /clone_lib="GRN_ES"
                     /note="oligo dT primed, full-length enriched cDNA library
                     from undifferentiated hES cell lines H1 (p32), H7 (p29),
                     and H9 (p26) maintained in feeder-free conditions"

ORIGIN

Qy Query Match   97.3%;   Score 14.6;   DB 7;   Length 417;
    Best Local Similarity   93.3%;   Pred. No. 5e+02;
    Matches 14;   Conservative 1;   Mismatches 0;   Indels 0;   Gaps 0;

Qy   1 GGTTCACSGATTGTC 15
          |||||||| ||||||
Db 184 GGTTCACCGGATTGTC 198

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RESULT 2
BF840993/c
LOCUS       BF840993        447 bp    mRNA    linear   EST 13-JAN-2001
DEFINITION  RC3-HT0974-011200-013-a03 HT0974 Homo sapiens cDNA, mRNA sequence.
ACCESSION   BF840993
VERSION     BF840993.1  GI:12193641
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 447)
AUTHORS     Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
            Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
            Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
            Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V.,
            O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
            Simpson,A.J.
TITLE       Shotgun sequencing of the human transcriptome with ORF expressed
            sequence tags
JOURNAL     Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
MEDLINE     20202663
PUBMED      10737800
COMMENT     Contact: Simpson A.J.G.
            Laboratory of Cancer Genetics
            Ludwig Institute for Cancer Research
            Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
            Brazil
            Tel: +55-11-2704922
            Fax: +55-11-2707001
            Email: asimpson@ludwig.org.br
            This sequence was derived from the FAPESP/LICR Human Cancer Genome
            Project. This entry can be seen in the following URL
            (http://www.ludwig.org.br/scripts/gethtml2.pl?ti=RC3&t2=RC3-HT0974-
            011200-013-a03&t3=2000-12-01&t4=1)
            Seq primer: puc 18 forward
            High quality sequence start: 29
            High quality sequence stop: 447.
FEATURES             Location/Qualifiers
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                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /dev_stage="Adult"
                     /clone_lib="HT0974"
                     /note="Organ: head neck; Vector: puc18; Site 1: SmaI;
                     Site 2: SmaI; A mini-library was made by cloning products
                     derived from ORESTES PCR (U.S. Letters Patent application
                     No. 196,716 - Ludwig Institute for Cancer Research)
                     profiles into the pUC 18 vector. Reverse transcription of
                     tissue mRNA and cDNA amplification were performed under
                     low stringency conditions."

Qy    1 GGTTCACSGATTGTC 15
         |||||||| |||||||
Db  319 GGTTCACGGATTGTC 305

RESULT 3
AL702133
LOCUS       AL702133        513 bp    mRNA    linear   EST 04-SEP-2003
DEFINITION  DKFZp686G02155_r1 686 (synonym: hlcc3) Homo sapiens cDNA clone
            DKFZp686G02155_5', mRNA sequence.
ACCESSION   AL702133
VERSION     AL702133.1  GI:19685488
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 513)
AUTHORS     Wiemann,S.
TITLE       EST (Bloecker,H., Boecher,M., Brandt,P., Mewes,H.W., Weil,B. and
            Wiemann,S.)
JOURNAL     Unpublished (1999)
COMMENT     Contact: MIPS
            MIPS
            Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany
            This is the 5' sequence of the clone insert
            Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
            Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
            sequenced by GBF (National Research Centre for Biotechnology Ltd.,
            Braunschweig/Germany) within the cDNA sequencing consortium of the
            German Genome Project.
            No si sequence available.
            This clone (DKFZp686G02155) is available at the RZPD in Berlin.
            Please contact the RZPD: Resourcenzentrum, Heubnerweg 6, 14059
            Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.
FEATURES             Location/Qualifiers
     source          1..513
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="DKFZp686G02155"
                     /dev_stage="adult"
                     /lab_host="DH10B"
                     /clone_lib="686 (synonym: hlcc3)"
                     /note="Vector: pTriplEx2; Site_1: SfiIA; Site_2: SfiIB;
                     cDNA-collection"

Qy    1 GGTTCACSGATTGTC 15
         |||||||| |||||||
Db  292 GGTTCACGGATTGTC 306

RESULT 4
BI647985/c
LOCUS       BI647985        524 bp    mRNA    linear   EST 12-SEP-2001
DEFINITION  603276059F1 NCI_CGAP_Mam3 Mus musculus cDNA clone IMAGE:5316470 5',
            mRNA sequence.
ACCESSION   BI647985
VERSION     BI647985.1  GI:15562208
KEYWORDS    EST.
SOURCE      Mus musculus (house mouse)
ORGANISM    Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 524)
AUTHORS     NIH-MGC http://mgc.nci.nih.gov/.
TITLE       National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL     Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Lothar Hennighausen Ph.D., Chu-Xia Deng Ph.D.
            cDNA Library Preparation: Life Technologies, Inc.
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Incyte Genomics, Inc.
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM11802  row: e  column: 15
            High quality sequence start: 196
            High quality sequence stop: 522.
FEATURES             Location/Qualifiers
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Query Match   97.3%; Score 14.6; DB 2; Length 447;
Best Local Similarity 93.3%; Pred. No. 5.1e+02;
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Query Match   97.3%; Score 14.6; DB 1; Length 513;
Best Local Similarity 93.3%; Pred. No. 5.1e+02;
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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QM nucleic - nucleic search, using sw model

                     GenCore version 5.1.6
                     Copyright (c) 1993 - 2005 Compugen Ltd.

Run on:          July 31, 2005, 14:44:02 ; Search time 546.895 Seconds
                                          (without alignments)
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Title:
Perfect score:   19
Sequence:        1 gccagtgtttgcctgag 19

Scoring table:   IDENTITY_NUC
                 Gapop 10.0 , Gapext 1.0
Searched:        4708233 seqs, 2422707955 residues

Total number of hits satisfying chosen parameters:        9416466

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :       GenEmbl:*
                 1: gb_ba:*
                 2: gb_htg:*
                 3: gb_in:*
                 4: gb_om:*
                 5: gb_ov:*
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                 7: gb_ph:*
                 8: gb_pl:*
                 9: gb_pr:*
                10: gb_ro:*
                11: gb_sts:*
                12: gb_sy:*
                13: gb_un:*
                14: gb_vi:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

                                    SUMMARIES

                                 %
Result            Query
No.     Score   Match  Length  DB  ID           Description
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   1      19   100.0      19    6  AX676129     AX676129 Sequence
   2      19   100.0    3516    6  CQ724004     CQ724004 Sequence
   3      19   100.0    3999    6  AR070165     AR070165 Sequence
   4      19   100.0    3999    6  AR124807     AR124807 Sequence
   5      19   100.0    4417    6  CQ850139     CQ850139 Sequence
   6      19   100.0    4417    9  AK127237     AK127237 Homo sapi
   7      19   100.0    4788    6  BD156525     BD156525 Primer fo
   8      19   100.0    4788    9  AX877177     AX877177 Sequence
   9      19   100.0    4788    6  AK001641     AK001641 Homo sapi
  10      19   100.0    4803    6  BD171366     BD171366 Method fo
  11      19   100.0    4803    6  BD173600     BD173600 Method of
  12      19   100.0    4803    6  AX210634     AX210634 Sequence
  13      19   100.0    4803    9  AF044195     AF044195 Homo sapi
  14      19   100.0    5047    6  BC033094     BC033094 Homo sapi
  15      19   100.0    5924    6  AX676049     AX676049 Sequence
  16      19   100.0    5924    9  AF153419     AF153419 Homo sapi
  17      19   100.0    6479    9  AX676048     AX676048 Homo sapi
  18      19   100.0    7876    9  AL359692     AL359692 Human DNA
  19      18    94.7     392    6  AX210429     AX210429 Sequence

  20      18    94.7   181675    2  AC113990     AC113990 Mus muscu
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  23      17.4   91.6  116636    9  AL096772     AL096772 Human DNA
  24      17.4   91.6  158391   10  AC115051     AC115051 Mus muscu
  25      17.4   91.6  164603    2  AC119466     AC119466 Rattus no
  26      17.4   91.6  180338   10  AC090496     AC090496 Mus muscu
  27      17.4   91.6  186113    9  AC116697     AC116697 Mus muscu
  28      17.4   91.6  186613    9  AC129097     AC129097 Papio anu
  29      17.4   91.6  219340   10  AL844881     AL844881 Mouse DNA
  30      17.4   91.6  219714    2  AC096601     AC096601 Rattus no
  31      17.4   91.6  223996    2  AC094504     AC094504 Rattus no
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  33      17.4   91.6  267540    2  AC107153     AC107153 Rattus no
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  37      17      89.5  150641    9  AC092153     AC092153 Homo sapi
  38      17      89.5  151046   10  AC104598     AC104598 Homo sapi
  39      17      89.5  189666   10  AC131104     AC131104 Mus muscu
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  41      17      89.5  201478   10  AC118442     AC118442 Rattus no
  42      17      89.5  204478   10  AC132608     AC132608 Mus muscu
  43      17      89.5  234795   10  AC099934     AC099934 Mus muscu
  44      17      89.5  235978    2  AC116249     AC116249 Rattus no
  45      17      89.5  243910    2  AC096208     AC096208 Rattus no
  45      17      89.5  317634    2  AC150936     AC150936 Bos tauru


                                   ALIGNMENTS

RESULT 1
LOCUS       AX676129                   19 bp    DNA     linear    PAT 27-MAR-2003
DEFINITION  Sequence 82 from Patent WO02059381.
ACCESSION   AX676129
VERSION     AX676129.1   GI:29333813
KEYWORDS
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Slaugenhaupt,S. and Gusella,J.F.
  TITLE     Gene for identifying individuals with familial dysautonomia
  JOURNAL   Patent: WO 02059381-A 82 01-AUG-2002;
            The General Hospital Corporation (US)
FEATURES             Location/Qualifiers
     source          1..19
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                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
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ORIGIN

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Qy          1 GCCAGTGTTTGCCTGAG 19
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Db          1 GCCAGTGTTTGCCTGAG 19

RESULT 2
LOCUS       CQ724004                 3516 bp    DNA     linear    PAT 03-FEB-2004
DEFINITION  Sequence 9938 from Patent WO02068579.
ACCESSION   CQ724004
VERSION     CQ724004.1   GI:42284861
KEYWORDS
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
```

```
                Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Venter,C.J., Adams,M.C., Li,P.W. and Myers,E.W.
  TITLE     kits, such as nucleic acid arrays, comprising a majority of
            humans or transcripts, for detecting expression and other uses
            thereof
  JOURNAL   Patent: WO 02068579-A 9938 06-SEP-2002;
            PE Corporation (NY) (US)
FEATURES
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RESULT 3
LOCUS       AR070165     3999 bp   DNA    linear   PAT 18-FEB-2000
DEFINITION  Sequence 1 from patent US 5891719.
ACCESSION   AR070165
VERSION     AR070165.1  GI:7221053
KEYWORDS
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 3999)
  AUTHORS   Cohen,L. and Baeuerle,P.
  TITLE     IKAP nucleic acids
  JOURNAL   Patent: US 5891719-A 1 06-APR-1999;
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Qy     1 GCCAGTGTTTTTTGCCTGAG 19
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Db  1979 GCCAGTGTTTTTTGCCTGAG 1997


RESULT 4
LOCUS       AR124807     3999 bp   DNA    linear   PAT 16-MAY-2001
DEFINITION  Sequence 1 from patent US 6172195.
ACCESSION   AR124807
VERSION     AR124807.1  GI:14110168
KEYWORDS
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 3999)
  AUTHORS   Cohen,L. and Baeuerle,P.
  TITLE     IKAP proteins and methods
  JOURNAL   Patent: US 6172195-A1 09-JAN-2001;
FEATURES
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                  /mol_type="unassigned DNA"
ORIGIN

Qy  Query Match  100.0%;  Score 19;  DB 6;  Length 3999;
Db  Best Local Similarity  100.0%;  Pred. No. 29;
    Matches 19;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;

Qy     1 GCCAGTGTTTTTTGCCTGAG 19
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Db  1979 GCCAGTGTTTTTTGCCTGAG 1997


RESULT 5
LOCUS       CQ850139     4417 bp   DNA    linear   PAT 23-AUG-2004
DEFINITION  Sequence 608 from Patent EP1447413.
ACCESSION   CQ850139
VERSION     CQ850139.1  GI:51508351
KEYWORDS
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Isogai,T., Yamamoto,J., Nishikawa,T., Isono,Y., Sugiyama,T.,
            Otsuki,T., Wakamatsu,A., Ishii,S., Nagai,K. and Irie,R.
  TITLE     Full-length human cDNA
  JOURNAL   Patent: EP 1447413-A 608 18-AUG-2004;
            Research Association for Biotechnology (JP)
FEATURES
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ORIGIN

Qy  Query Match  100.0%;  Score 19;  DB 6;  Length 4417;
Db  Best Local Similarity  100.0%;  Pred. No. 29;
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Qy     1 GCCAGTGTTTTTTGCCTGAG 19
         ||||||||||||||||||||
Db  1918 GCCAGTGTTTTTTGCCTGAG 1936


RESULT 6
LOCUS       AK127237     4417 bp   mRNA   linear   PRI 19-FEB-2004
DEFINITION  Homo sapiens cDNA FLJ45304 fis, clone BRHIP3003984, highly similar
            to IkappaB kinase complex-associated protein.
ACCESSION   AK127237
VERSION     AK127237.1  GI:34534066
KEYWORDS    oligo capping; fis (full insert sequence).
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Oshima,A., Takahashi-Fujii,A., Tanase,T., Imose,N., Takeuchi,K.,
            Arita,M., Musashino,K., Yuuki,H., Hara,H., Sugiyama,T., Irie,R.,
            Otsuki,T., Sato,H., Wakamatsu,A., Ishii,S., Yamamoto,J., Isono,Y.,
            Kawai-Hio,Y., Saito,K., Nishikawa,T., Kimura,K., Yamashita,H.,
            Matsuo,K., Nakamura,Y., Sekine,M., Kikuchi,H., Kanda,K.,
            Wagatsuma,M., Murakawa,K., Kanehori,K., Sugiyama,A., Kawakami,B.,
            Suzuki,Y., Sugano,S., Nagahari,K., Masuho,Y., Nagai,K. and
            Isogai,T.
  TITLE     NEDO human cDNA sequencing project
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 4417)
  AUTHORS   Isogai,T. and Yamamoto,J.
  TITLE     Direct Submission
  JOURNAL   Submitted (15-JUL-2003) Takao Isogai, FLJ Project(HRI Team); 2-6-7
            Kazusa-Kamatari, Kisarazu, Chiba 292-0818, Japan
            (E-mail:genomics@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986)
COMMENT     NEDO human cDNA sequencing project supported by Ministry of
            Economy, Trade and Industry of Japan; cDNA full insert sequencing:
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OM nucleic - nucleic search, using sw model

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Pred. No. is the number of results predicted by chance to have a
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and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
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3	19	100.0	3999	4	AAF29756	Aaf29756 Human IKA
4	19	100.0	4417	13	ADR07102	Adr07102 Full leng
5	19	100.0	4788	4	AAH14533	Aah14533 Human cDN
6	19	100.0	4803	6	AAH81767	Aah81767 Human dif
7	19	100.0	4803	6	AAL44190	Aal44190 Human I-k
8	19	100.0	5924	6	ABQ80570	Abq80570 Mutant hu
9	19	100.0	5924	6	ABQ80569	Abq80569 Human IKB
10	19	100.0	5924	8	ACD13384	Acd13384 Human DNA
11	19	100.0	6479	6	ABQ80567	Abq80567 Mutant hu
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13	19	100.0	6479	6	ABQ80568	Abq80568 Mutant hu
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17	16.4	86.3	5550	4	ABL08413	Abl08413 Drosophil
18	16.4	86.3	7887	4	ABL08412	Abl08412 Drosophil
19	16.4	86.3	14417	10	ABZ77045	Abz77045 Bovine DG
20	16.4	86.3	14117	10	ABZ77044	Abz77044 Bovine DG
21	16	84.2	432	8	ABX43560	Abx43560 Bovine ES
22	16	84.2	770	2	AAV28664	Aav28664 Ripening
23	16	84.2	180550	10	ADI13850	Adi13850 Osteoarth
24	15.8	83.2	20	2	AAZ03131	Aaz03131 PCR prime
25	15.8	83.2	171	8	ABZ19361	Abz19361 Group III
26	15.8	83.2	202	4	AAI24501	Aai24501 Human bre
27	15.8	83.2	203	11	ADT97815	Adt97815 Colon can
28	15.8	83.2	259	4	AAI15657	Aai15657 Human bre
29	15.8	83.2	1011	2	AAZ27728	Aaz27728 Human DNA
30	15.8	83.2	1011	2	AAZ27729	Aaz27729 Human DNA
31	15.8	83.2	1271	11	ACN85637	Acn85637 Breast ca
32	15.8	83.2	1519	6	ABK34935	Abk34935 Human cDN
33	15.8	83.2	1665	3	AAC47898	Aac47898 Arabidops
34	15.8	83.2	2488	10	ADB62749	Adb62749 Human CDN
35	15.8	83.2	2495	8	ABT32174	Abt32174 Human neu
36	15.8	83.2	2547	4	AAH13749	Aah13749 Human CDN
37	15.8	83.2	2666	13	ABD33352	Abd33352 Murine ca
38	15.8	83.2	3788	4	AAS33107	Aas33107 DNA encod
39	15.8	83.2	4463	2	AAV62085	Aav62085 Thermococ
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41	15.8	83.2	6057	8	ABX63239	Abx63239 Human cDN
42	15.8	83.2	6111	13	ACN40249	Acn40249 Tumour-as
43	15.8	83.2	6330	5	ABV30125	Abv30125 Human pro
44	15.8	83.2	6342	11	ACN92292	Acn92292 Breast ca
45	15.8	83.2	9528	4	ABL19946	Abl19946 Drosophil

ALIGNMENTS

RESULT 1
ABQ80558

ID   ABQ80558 standard; DNA; 19 BP.
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AC   ABQ80558;
XX
DT   08-NOV-2002 (first entry)
XX
DE   IKBKAP PCR primer 18F.
XX
KW   Human; IKBKAP; Familial Dysautonomia; FD; Riley-Day syndrome;
KW   Hereditary Sensory and Autonomic Neuropathy Type III; carrier screening;
KW   PCR; primer; ss.
XX
OS   Homo sapiens.
XX
PN   WO200259381-A2.
XX
PD   01-AUG-2002.
XX
PF   07-JAN-2002; 2002WO-US000473.
XX
PR   06-JAN-2001; 2001US-0260080P.
XX
PA   (GEHO) GEN HOSPITAL CORP.
XX
PI   Slaugenhaupt S, Gusella JF;
XX
DR   WPI; 2002-674806/72.
XX
PT   New IKBKAP genes with mutations, useful for identifying a subject with
PT   familial dysautonomia (FD), or for rapid carrier screening in the
PT   Ashkenazi Jewish population, e.g. screening presymptomatic homozygotes or
PT   prenatal diagnosis.
XX
PS   Claim 33; Page 27; 109pp; English.
XX
CC   The present invention relates to methods and compositions useful for
CC   detecting mutations which cause Familial Dysautonomia (FD, Riley-Day
CC   syndrome, Hereditary Sensory and Autonomic Neuropathy Type III) [OMIM
CC   223900]. It was found that mutations in the IKBKAP gene (see ABQ80565)
CC   are associated with FD. The mutation associated with the major haplotype
CC   of FD, FD1 mutation, is a base pair (bp) mutation, where the thymine

```
CC   nucleotide located at bp 6 of intron 20 in the IKBKAP gene is replaced
CC   with a cytosine. This results in skipping of exon 20 in the mRNA from FD
CC   patients, although they continue to express varying levels of wild-type
CC   message in a tissue-specific manner. The mutation associated with the
CC   minor haplotype, FD2 mutation, is a bp mutation, where the guanine
CC   nucleotide at bp 2397 (bp 73 of exon 19) is replaced with a cytosine.
CC   This bp mutation causes an arginine to proline missense mutation (R696P)
CC   in the IKBKAP protein, which is predicted to disrupt a potential
CC   phosphorylation site. The IKBKAP nucleic acid sequences are useful for
CC   identifying a subject with FD and for rapid carrier screening. The IKBKAP
CC   gene maps to chromosome 9q31. PCR primers ABQ80558-ABQ80560 were used to
CC   detect the splicing defect in IKBKAP gene
XX
SQ   Sequence 19 BP; 2 A; 4 C; 6 G; 7 T; 0 U; 0 Other;

Qy          1 GCCAGTGTTTTTGCCTGAG 19
              |||||||||||||||||||
Db          1 GCCAGTGTTTTTGCCTGAG 19

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Best Local Similarity   100.0%;  Pred. No. 14;
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AC   AAX28025;
XX
DT   09-JUN-1999  (first entry)
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DE   Human IKAP coding sequence.
XX
KW   IKAP; human; cellular signal transduction regulator;
KW   transcriptional activation regulator; translatable transcript; ds.
XX
OS   Homo sapiens.
XX
PN   US5891719-A.
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PD   06-APR-1999.
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PF   16-NOV-1997;  97US-00971244.
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PR   16-NOV-1997;  97US-00971244.
XX
PA   (TULA-) TULARIK INC.
XX
PI   Cohen L,  Baeuerle P;
XX
DR   WPI; 1999-253865/21.
DR   P-PSDB; AAY01084.
XX
PT   Isolated, recombinant cDNA sequences encoding human IKAP polypeptides -
PT   useful for regulating cellular signal transduction and transcriptional
PT   activation.
XX
PS   Claim 23; Col 9-18; 15pp; English.
XX
CC   This sequence encodes the human IKAP protein of the invention. IKAP
CC   regulates cellular signal transduction and transcriptional activation
CC   (e.g. the activation of nuclear factor kappaB). Nucleic acids encoding
CC   IKAP have a range of applications including use as translatable
CC   transcripts, hybridisation probes, polymerase chain reaction (PCR)
CC   primers, diagnostic nucleic acids, use in detecting the presence of IKAP
CC   genes and gene transcripts and in detecting or amplifying nucleic acids
CC   encoding additional IKAP homologues and structural analogues. In
CC   diagnosis IKAP hybridisation probes may be used to identify wild-type and
CC   mutant IKAP alleles in clinical samples. In therapy, IKAP nucleic acids
CC   can be used to modulate cellular expression or intracellular
CC   concentration or availability of active IKAP
XX
SQ   Sequence 3999 BP; 1110 A; 851 C; 995 G; 1043 T; 0 U; 0 Other;

Qy          1 GCCAGTGTTTTTGCCTGAG 19
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Db       1979 GCCAGTGTTTTTGCCTGAG 1997

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Best Local Similarity   100.0%;  Pred. No. 25;
Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

RESULT 3
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ID   AAF29756 standard; cDNA; 3999 BP.
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AC   AAF29756;
XX
DT   05-APR-2001  (first entry)
XX
DE   Human IKAP coding sequence.
XX
KW   IKAP; signal transduction; NIK binding activity;
KW   transcription factor; diagnosis; therapy; ss.
XX
OS   Homo sapiens.
XX
PN   US6172195-B1.
XX
PD   09-JAN-2001.
XX
PF   06-APR-1999;  99US-00286891.
XX
PR   16-NOV-1997;  97US-00971244.
XX
PA   (TULA-) TULARIK INC.
XX
PI   Cohen L,  Baeuerle P;
XX
DR   WPI; 2001-158378/16.
DR   P-PSDB; AAB66345.
XX
PT   Novel human kinase IKAP polypeptide useful in diagnosis, therapy,
PT   biopharmaceutical industry and for screening for modulators of the
PT   polypeptide.
XX
PS   Disclosure; Col 9-18; 15pp; English.
XX
CC   The present invention provides the human IKAP protein. This is involved
CC   in signal transduction pathways, where it binds to NIK and results in the
CC   activation of transcription factors. The protein and its coding sequence
CC   can be used in disease diagnosis and therapy, as well as in the
CC   biopharmaceutical industry
XX
SQ   Sequence 3999 BP; 1110 A; 851 C; 995 G; 1043 T; 0 U; 0 Other;

Qy          1 GCCAGTGTTTTTGCCTGAG 19
              |||||||||||||||||||
Db       1979 GCCAGTGTTTTTGCCTGAG 1997

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Best Local Similarity   100.0%;  Pred. No. 25;
Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

RESULT 4
ADR07102
ID   ADR07102 standard; cDNA; 4417 BP.
XX
AC   ADR07102;
XX
DT   04-NOV-2004  (first entry)
XX
DE   Full length human cDNA useful for treating neurological disease Seq 608.
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OM nucleic - nucleic search, using sw model

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GenCore version 5.1.6

Run on: July 31, 2005, 14:57:07 ; Search time 39.2901 Seconds
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Title: US-10-041-856-82
Perfect score: 19
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Searched: 1202784 seqs, 81818359 residues

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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2	19	100.0	3999	4	US-09-286-891-1	Sequence 1, Appli
3	15.8	83.2	601	4	US-09-949-016-68848	Sequence 68848, A
4	15.8	83.2	601	4	US-09-949-016-68849	Sequence 68849, A
5	15.8	83.2	1011	3	US-09-018-584A-28	Sequence 28, Appl
6	15.8	83.2	1011	3	US-09-018-584A-29	Sequence 29, Appl
7	15.8	83.2	1011	4	US-09-784-423-28	Sequence 28, Appl
8	15.8	83.2	1011	4	US-09-784-423-29	Sequence 29, Appl
9	15.8	83.2	4463	2	US-08-760-489-1	Sequence 1, Appli
10	15.8	83.2	4463	3	US-08-760-489-1	Sequence 1, Appli
11	15.8	83.2	4463	3	US-09-185-373-1	Sequence 1, Appli
12	15.8	83.2	4463	3	US-09-185-373-3	Sequence 3, Appli
13	15.8	83.2	128470	4	US-09-949-016-13765	Sequence 13765, A
14	15.8	83.2	601	4	US-09-949-016-29141	Sequence 29141, A
15	15.8	83.2	601	4	US-09-949-016-41096	Sequence 41096, A
16	15.8	83.2	858	3	US-09-334-938-12	Sequence 12, Appl
17	15.8	81.1	909	4	US-09-252-991A-7481	Sequence 7481, Ap
18	15.4	81.1	1149	4	US-09-252-991A-7156	Sequence 7156, Ap
19	15.4	81.1	1335	4	US-09-252-991A-7421	Sequence 7421, Ap
20	15.4	81.1	2667	4	US-09-252-991A-7216	Sequence 7216, Ap
21	15.4	81.1	16073	4	US-09-949-016-12312	Sequence 12312, A
22	15.4	81.1	16073	4	US-09-949-016-12905	Sequence 12905, A
23	15.4	81.1	45862	4	US-09-949-016-13928	Sequence 13928, A
24	15.4	81.1	102008	4	US-09-949-016-16617	Sequence 16617, A
25	15	78.9	396	4	US-09-513-999C-13741	Sequence 13741, A
26	15	78.9	855	4	US-09-949-016-1607	Sequence 1607, Ap
27	15	78.9	855	4	US-09-949-016-1608	Sequence 1608, Ap
28	15	78.9	7130	3	US-09-056-105-31	Sequence 31, Appl
29	15	78.9	9245	4	US-09-949-016-13349	Sequence 13349, A
30	15	78.9	9245	4	US-09-949-016-13350	Sequence 13350, A
31	15	78.9	42741	4	US-09-949-016-11857	Sequence 11857, A
32	15	78.9	150394	4	US-09-949-016-13042	Sequence 13042, A
33	14.8	77.9	65	1	US-08-105-483-124	Sequence 124, App
34	14.8	77.9	65	1	US-07-714-687-37	Sequence 37, Appl
35	14.8	77.9	65	1	US-08-224-391-37	Sequence 37, Appl
36	14.8	77.9	65	1	US-08-484-304-37	Sequence 37, Appl
37	14.8	77.9	65	1	US-08-709-209-124	Sequence 124, App
38	14.8	77.9	65	1	US-09-949-016-11124	Sequence 124, App
39	14.8	77.9	65	1	US-08-458-101-124	Sequence 124, App
40	14.8	77.9	65	1	US-08-105-483-123	Sequence 123, App
41	14.8	77.9	65	1	US-07-714-687-36	Sequence 36, Appl
42	14.8	77.9	65	1	US-08-224-391-36	Sequence 36, Appl
43	14.8	77.9	65	1	US-08-484-304-36	Sequence 36, Appl
44	14.8	77.9	69	1	US-08-709-209-123	Sequence 123, App
45	14.8	77.9	117	1	US-08-299-498A-76	Sequence 76, Appl

ALIGNMENTS

RESULT 1
US-08-971-244-1
Sequence 1, Application US/08971244
Patent No. 5891719
GENERAL INFORMATION:
; APPLICANT: Cohen, Lucy
; APPLICANT: Baeuerle, Patrick
; TITLE OF INVENTION: IKAP Proteins, Nucleic Acids and Methods
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
; STREET: 75 DENISE DRIVE
; CITY: HILLSBOROUGH
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94010
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/971,244
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: OSMAN, RICHARD A
; REGISTRATION NUMBER: 36,627
; REFERENCE/DOCKET NUMBER: T97-011
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 343-4341
; TELEFAX: (650) 343-4342
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3999 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..3996
US-08-971-244-1

Query Match   100.0%; Score 19; DB 2; Length 3999;
Best Local Similarity   100.0%; Pred. No. 6.7;
Matches   19; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   1 GCCAGTGTTTTTGCCTGAG 19
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RESULT 2
US-09-286-891-1
; Sequence 1, Application US/09286891
; Patent No. 6172195
; GENERAL INFORMATION:
; APPLICANT: Cohen, Lucy
; APPLICANT: Baeuerle, Patrick
; TITLE OF INVENTION: IKAP Proteins, Nucleic Acids and Methods
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
; STREET: 75 DENISE DRIVE
; CITY: HILLSBOROUGH
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94010
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/286,891
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/971,244
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: OSMAN, RICHARD A
; REGISTRATION NUMBER: 36,627
; REFERENCE/DOCKET NUMBER: T97-011
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 343-4342
; TELEFAX: (650) 343-4341
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3999 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..3996
US-09-286-891-1

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Best Local Similarity   100.0%; Pred. No. 6.7;
Matches   19; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

RESULT 3
US-09-949-016-68848
; Sequence 68848, Application US/0994016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768

; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 68848
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-68848

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; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 68849
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-68849

Qy   1 GCCAGTGTTTTTGCCTGAG 19
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Db   91 GCCAGTGTTTTTGGGCCTTAG 109

Query Match   83.2%; Score 15.8; DB 4; Length 601;
Best Local Similarity   89.5%; Pred. No. 2e+02;
Matches   17; Conservative   0; Mismatches   2; Indels   0; Gaps   0;

RESULT 5
US-09-018-584A-28/c
; Sequence 28, Application US/09018584A
; Patent No. 6238863
; GENERAL INFORMATION:
; APPLICANT: Schumm, James W.
; APPLICANT: Bacher, Jeffery W.
; TITLE OF INVENTION: MATERIALS AND METHODS FOR
; TITLE OF INVENTION: IDENTIFYING AND ANALYZING INTERMEDIATE TANDEM
; TITLE OF INVENTION: REPEAT DNA MARKERS
; NUMBER OF SEQUENCES: 147
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Promega Corporation
; STREET: 2800 Woods Hollow Road
; CITY: Madison
; STATE: Wisconsin
; COUNTRY: U.S.A.
; ZIP: 53711-5399
; COMPUTER READABLE FORM:

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Run on: July 31, 2005, 16:38:33 ; Search time 193.988 Seconds
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Perfect score: 19
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Searched: 7287783 seqs, 3236178273 residues
Total number of hits satisfying chosen parameters: 14575566

Post-processing: Minimum Match 0%
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Minimum DB seq length: 0
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Listing first 45 summaries

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10	19	100.0	201	20	US-10-719-993-4614	Sequence 4614, Ap
11	19	100.0	201	20	US-10-719-993-4620	Sequence 4620, Ap
12	19	100.0	201	20	US-10-719-993-34840	Sequence 34840, A
13	19	100.0	201	20	US-10-719-993-34842	Sequence 34842, A
14	19	100.0	201	20	US-10-719-993-34877	Sequence 34877, A
15	19	100.0	201	20	US-10-719-993-34940	Sequence 34940, A
16	19	100.0	201	20	US-10-719-993-319	Sequence 319, App
17	19	100.0	5840	21	US-10-956-157-1094	Sequence 1094, Ap
18	19	100.0	4803	20	US-10-719-993-322	Sequence 322, App
19	19	100.0	4803	10	US-10-041-856-2	Sequence 2, Appli
20	19	100.0	4256	20	US-10-719-993-320	Sequence 320, App
21	19	100.0	201	20	US-10-719-993-321	Sequence 321, App
22	19	100.0	201	20	US-10-719-993-318	Sequence 318, App
23	19	100.0	66479	13	US-10-041-856-1	Sequence 1, Appli
24	19	100.0	78878	20	US-10-719-999-6863	Sequence 6863, Ap
25	19	100.0	392	13	US-09-930-213-71	Sequence 71, Appl
26	18	94.7	392	10	US-10-027-632-44690	Sequence 44690, A
27	17.4	91.6	656	13	US-10-027-632-44690	Sequence 44690, A
28	17.4	91.6	656	17	US-10-723-860-4189	Sequence 4189, Ap
29	17.4	91.6	482	20	US-10-482-936-3	Sequence 3, Appli
30	16.4	86.3	14117	20	US-10-482-936-1	Sequence 1, Appli
31	16.4	86.3	14117	20	US-10-027-632-174961	Sequence 174961,
32	16.4	86.3	14117	13	US-10-027-632-174961	Sequence 174961,
33	16.4	86.3	3186778	13	US-09-960-352-8725	Sequence 8725, Ap
34	16	84.2	3186778	9	US-09-966-881-22	Sequence 22, Appl
35	16	84.2	432	9	US-10-242-535A-40898	Sequence 40898, A
36	16	84.2	770	17	US-10-066-543-3334	Sequence 3334, Ap
37	15.8	83.2	203	14	US-10-424-599-12632	Sequence 12632, A
38	15.8	83.2	189	18	US-10-242-535A-57294	Sequence 57294, A
39	15.8	83.2	189	17	US-10-242-535A-57294	Sequence 57294, A
40	15.8	83.2	467	18	US-10-085-783A-57294	Sequence 57294, A
41	15.8	83.2	473	17	US-10-242-535A-56824	Sequence 56824, A
42	15.8	83.2	473	18	US-10-085-783A-56824	Sequence 56824, A
43	15.8	83.2	480	17	US-10-242-535A-56824	Sequence 56824, A
44	15.8	83.2	480	17	US-10-242-535A-46356	Sequence 56356, A
45	15.8	83.2	594	18	US-10-085-783A-46356	Sequence 46356, A

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	19	100.0	19	13	US-10-041-856-82	Sequence 82, Appl
2	19	100.0	201	20	US-10-719-993-4501	Sequence 4501, Ap
3	19	100.0	201	20	US-10-719-993-4507	Sequence 4507, Ap
4	19	100.0	201	20	US-10-719-993-4528	Sequence 4528, Ap
5	19	100.0	201	20	US-10-719-993-4534	Sequence 4534, Ap
6	19	100.0	201	20	US-10-719-993-4557	Sequence 4557, Ap
7	19	100.0	201	20	US-10-719-993-4563	Sequence 4563, Ap

ALIGNMENTS

RESULT 1
US-10-041-856-82
Sequence 82, Application US/10041856
Publication No. US20020169299A1
GENERAL INFORMATION:
APPLICANT: SLAUGENHAUPT, SUSAN
APPLICANT: GUSELLA, JAMES F.
TITLE OF INVENTION: GENE FOR IDENTIFYING INDIVIDUALS WITH FAMILIAL
TITLE OF INVENTION: DYSAUTONOMIA
FILE REFERENCE: 1829-4004US1
CURRENT APPLICATION NUMBER: US/10/041,856
CURRENT FILING DATE: 2002-07-08
PRIOR APPLICATION NUMBER: 60/260,080
PRIOR FILING DATE: 2001-01-06
NUMBER OF SEQ ID NOS: 88
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 82
LENGTH: 19
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Primer
US-10-041-856-82

Query Match 100.0%; Score 19; DB 13; Length 19;
Best Local Similarity 100.0%; Pred. No. 9.5;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db   1 GCCAGTGTTTTTGCCTGAG 19

RESULT 2
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; Sequence 4501, Application US/10719993
; Publication No. US20040265849A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: ALZHEIMER'S DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001496
; CURRENT APPLICATION NUMBER: US/10/719,993
; CURRENT FILING DATE: 2003-11-24
; NUMBER OF SEQ ID NOS: 55342
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 4501
; LENGTH: 201
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-719-993-4501

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Best Local Similarity 100.0%;   Pred. No. 12;
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Db   154 GCCAGTGTTTTTGCCTGAG 172

RESULT 3
US-10-719-993-4507
; Sequence 4507, Application US/10719993
; Publication No. US20040265849A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: ALZHEIMER'S DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001496
; CURRENT APPLICATION NUMBER: US/10/719,993
; CURRENT FILING DATE: 2003-11-24
; NUMBER OF SEQ ID NOS: 55342
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 4507
; LENGTH: 201
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-719-993-4507

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Best Local Similarity 100.0%;   Pred. No. 12;
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RESULT 4
US-10-719-993-4528
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; Publication No. US20040265849A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: ALZHEIMER'S DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001496
; CURRENT APPLICATION NUMBER: US/10/719,993
; CURRENT FILING DATE: 2003-11-24
; NUMBER OF SEQ ID NOS: 55342
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 4528
; LENGTH: 201
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-719-993-4528

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Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db   154 GCCAGTGTTTTTGCCTGAG 172

RESULT 5
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; Publication No. US20040265849A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: ALZHEIMER'S DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001496
; CURRENT APPLICATION NUMBER: US/10/719,993
; CURRENT FILING DATE: 2003-11-24
; NUMBER OF SEQ ID NOS: 55342
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 4534
; LENGTH: 201
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-719-993-4534

Query Match   100.0%;   Score 19; DB 20; Length 201;
Best Local Similarity 100.0%;   Pred. No. 12;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db   154 GCCAGTGTTTTTGCCTGAG 172

RESULT 6
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; Publication No. US20040265849A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: ALZHEIMER'S DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001496
; CURRENT APPLICATION NUMBER: US/10/719,993
; CURRENT FILING DATE: 2003-11-24
; NUMBER OF SEQ ID NOS: 55342
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 4557
; LENGTH: 201
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-719-993-4557

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Db   115 GCCAGTGTTTTTGCCTGAG 133

RESULT 7
US-10-719-993-4563
; Sequence 4563, Application US/10719993

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: July 31, 2005, 15:46:58 ; Search time 930.414 Seconds
                                                (without alignments)
                                                777.311 Million cell updates/sec

Title: US-10-041-856-82
Perfect score: 19
Sequence: 1 gccagtgttttgcctgag 19
Scoring table: IDENTITY_NUC
                Gapop 10.0 , Gapext 1.0
Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   EST:*
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                2: gb_est2:*
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                5: gb_est4:*
                6: gb_est5:*
                7: gb_est6:*
                8: gb_gss1:*
                9: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.		Score	% Query Match	Length	DB	ID		Description
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2	c	19	100.0	417	7	CN256146	CN256146	170005321
3	c	19	100.0	447	2	BF840993	BF840993	RC3-HT097
4	c	19	100.0	513	1	AL702133	AL702133	DKFZp686G
5		19	100.0	553	4	BM512007	BM512007	ij77d11.x
6		19	100.0	580	5	BP243833	BP243833	BP243833
7		19	100.0	618	4	BG395601	BG395601	602458222
8		19	100.0	709	7	CN256149	CN256149	170004241
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12		19	100.0	1134	7	CN641971	CN641971	ILLUMIGEN
13		19	100.0	3833	3	CR749385	CR749385	Homo sapi
14		19	100.0	3999	9	AY414501	AY414501	Homo sapi
15		19	100.0	3999	9	AY414502	AY414502	Pan trogl
16	c	18	94.7	392	1	AA324126	AA324126	EST127019
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ALIGNMENTS

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DEFINITION IL2-BT0734-041000-178-C01 BT0734 Homo sapiens cDNA, mRNA sequence.
ACCESSION   BF742852
VERSION   BF742852.1 GI:12069528
KEYWORDS   EST.
SOURCE   Homo sapiens (human)
  ORGANISM Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 412)
  AUTHORS   Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
            Nagi,M.A., da Silva,W.Jr., Zago,M.A., Bordin,S., Costa,F.F.,
            Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
            Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V.,
            O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
            Simpson,A.J.
  TITLE   Shotgun sequencing of the human transcriptome with ORF expressed
            sequence tags
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
   MEDLINE   20202663
   PUBMED   10737800
COMMENT   Contact: Simpson A.J.G.
            Laboratory of Cancer Genetics
            Ludwig Institute for Cancer Research
            Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
            Brazil
            Tel: +55-11-2704922
            Fax: +55-11-2707001
            Email: asimpson@ludwig.org.br
            This sequence was derived from the FAPESP/LICR Human Cancer Genome
            Project. This entry can be seen in the following URL
            (http://www.ludwig.org.br/scripts/gethtml2.pl?ti=IL2&t2=IL2-BT0734-
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                     /dev_stage="Adult"
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ORIGIN

196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

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Qy          1 GCCAGTGTTTTTGCCTGAG 19
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Db        100 GCCAGTGTTTTTGCCTGAG 82
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RESULT 2

LOCUS   CN256146   417 bp   mRNA   linear   EST 16-MAY-2004
DEFINITION   1700032188935 GRN_ES Homo sapiens cDNA 5', mRNA sequence.
ACCESSION   CN256146
VERSION   CN256146.1 GI:47272560
KEYWORDS   EST.
SOURCE   Homo sapiens (human)
  ORGANISM   Homo sapiens
             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
             Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 417)
  AUTHORS   Brandenberger,R., Wei,H., Zhang,S., Lei,S., Murage,J., Fisk,G.J.,
             Li,Y., Xu,C., Fang,R., Guegler,K., Rao,M.S., Mandalam,R.,
             Lebkowski,J and Stanton,L.W.
  TITLE   Transcriptome characterization elucidates signaling networks that
             control human ES cell growth and differentiation
  JOURNAL   Nat. Biotechnol. 22 (6), 707-716 (2004)
COMMENT   Contact: Brandenberger R
             Regenerative Medicine
             Geron Corporation
             230 Constitution Drive, Menlo Park, CA 94025, USA
             Tel: 650 473 8658
             Fax: 650 473 7760
             Email: rbrandenberger@geron.com
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                     and H9 (p26) maintained in feeder-free conditions"

ORIGIN

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Qy          1 GCCAGTGTTTTTGCCTGAG 19
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Db         83 GCCAGTGTTTTTGCCTGAG 101
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RESULT 3

LOCUS   BF840993   447 bp   mRNA   linear   EST 13-JAN-2001
DEFINITION   RC3-HT0974-011200-013-a03 HT0974 Homo sapiens cDNA, mRNA sequence.
ACCESSION   BF840993
VERSION   BF840993.1 GI:12193641
KEYWORDS   EST.
SOURCE   Homo sapiens (human)
  ORGANISM   Homo sapiens
             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Best Local Similarity   100.0%;
Matches   19; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Query Match   100.0%; Score 19; DB 2; Length 412;
Best Local Similarity   100.0%; Pred. No. 1.5e+02;
Matches   19; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

COMMENT   Contact: Simpson A.J.G.
             Laboratory of Cancer Genetics
             Ludwig Institute for Cancer Research
             Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
             Brazil
             Tel: +55-11-2704922
             Fax: +55-11-2707001
             Email: asimpson@ludwig.org.br
             This sequence was derived from the FAPESP/LICR Human Cancer Genome
             Project. This entry can be seen in the following URL
             (http://www.ludwig.org.br/scripts/getmtb12.pl?tis=RC3&t2=RC3-HT0974-
             011200-013-a03&t3=2000-12-01&t4=1)
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             High quality sequence stop: 447.
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                     /db_xref="taxon:9606"
                     /clone_lib="HT0974"
                     /note="Organ: head;neck; Vector: puc18; Site_1: SmaI;
                     Site_2: SmaI; A mini-library was made by cloning products
                     derived from ORESTES PCR (U.S. Letters Patent application
                     No. 196,716 - Ludwig Institute for Cancer Research)
                     profiles into the pUC 18 vector. Reverse transcription of
                     tissue mRNA and cDNA amplification were performed under
                     low stringency conditions."

ORIGIN

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Qy          1 GCCAGTGTTTTTGCCTGAG 19
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Db        420 GCCAGTGTTTTTGCCTGAG 402
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RESULT 4

LOCUS   AL702133   513 bp   mRNA   linear   EST 04-SEP-2003
DEFINITION   DKFZp686G02155_r1 686 (synonym: hlcc3) Homo sapiens cDNA clone
             DKFZp686G02155 5', mRNA sequence.
ACCESSION   AL702133
VERSION   AL702133.1 GI:19685488
KEYWORDS   EST.
SOURCE   Homo sapiens (human)
  ORGANISM   Homo sapiens
             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
             Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 513)
  AUTHORS   Wiemann,S., Bloecker,H., Boecher,M., Brandt,P., Mewes,W., Weil,B. and
             Wiemann,S.
  TITLE   EST (Bloecker,H., Boecher,M., Brandt,P., Mewes,H.W., Weil,B. and
             Wiemann,S.)
  JOURNAL   Unpublished (1999)
COMMENT   Contact: MIPS
             MIPS

Query Match   100.0%; Score 19; DB 7; Length 447;
Best Local Similarity   100.0%; Pred. No. 1.5e+02;
Matches   19; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

REFERENCE   1 (bases 1 to 447)
  AUTHORS   Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
             Nagai,M.A., da Silva,W., Jr., Zago,M.A., Bordin,S., Costa,F.F.,
             Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
             Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V.,
             O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
             Simpson,A.J.
  TITLE   Shotgun sequencing of the human transcriptome with ORF expressed
             sequence tags
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
   PUBMED   10737800
   MEDLINE   20202663
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OM nucleic - nucleic search, using sw model

GenCore version 5.1.6
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Run on: July 31, 2005, 14:44:02 ; Search time 546.895 Seconds
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Total number of hits satisfying chosen parameters: 9416466
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Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

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                 14: gb_vi:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	19	100.0	19	6	AX676130	AX676130 Sequence
2	19	100.0	803	6	BD147310	BD147310 Primer fo
3	19	100.0	803	6	AX867248	AX867248 Sequence
4	19	100.0	2471	6	BD157787	BD157787 Primer fo
5	19	100.0	2471	6	AX879348	AX879348 Sequence
6	19	100.0	2471	9	AK022559	AK022559 Homo sapi
7	19	100.0	3516	6	CQ724004	CQ724004 Sequence
8	19	100.0	3999	6	AR070165	AR070165 Sequence
9	19	100.0	3999	6	AR124807	AR124807 Sequence
10	19	100.0	4417	6	CQ850139	CQ850139 Sequence
11	19	100.0	4417	6	AK127237	AK127237 Homo sapi
12	19	100.0	4788	6	BD156525	BD156525 Primer fo
13	19	100.0	4788	6	AX877177	AX877177 Sequence
14	19	100.0	4788	6	AK001641	AK001641 Homo sapi
15	19	100.0	4803	6	BD171366	BD171366 Method fo
16	19	100.0	4803	6	BD173600	BD173600 Method of
17	19	100.0	4803	6	AX210634	AX210634 Sequence
18	19	100.0	4803	9	AF044195	AF044195 Homo sapi
19	19	100.0	5047	9	BC033094	BC033094 Homo sapi
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c 25	17.4	91.6	166062	2	AC146313	AC146313 Pongo pyg
c 26	17.4	91.6	176547	9	AC092447	AC092447 Homo sapi
c 27	17.4	91.6	184062	9	AC149232	AC149232 Pan trogl
c 28	17.4	91.6	191966	9	AC150280	AC150280 Pan trogl
c 29	17	89.5	151559	9	AL390294	AL390294 Human DNA
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c 32	16.4	86.3	25057	8	SPCP1E11	AL117183 S.pombe c
c 33	16.4	86.3	97057	9	AL627344	AL627344 Human DNA
c 34	16.4	86.3	111363	9	AC008606	AC008606 Homo sapi
c 35	16.4	86.3	116730	9	AC008548	AC008548 Homo sapi
c 36	16.4	86.3	151301	2	AL354717	AL354717 Homo sapi
c 37	16.4	86.3	156764	9	AC135268	AC135268 Rattus no
c 38	16.4	86.3	163781	9	AC058784	AC058784 Homo sapi
c 39	16.4	86.3	163910	9	AC145802	AC145802 Homo sapi
c 40	16.4	86.3	166950	9	AC113414	AC113414 Xenopus t
c 41	16.4	86.3	167227	9	CR759866	CR759866 Danio rer
c 42	16.4	86.3	168666	10	AC131085	AC131085 Mus muscu
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c 44	16.4	86.3	170141	2	AC015479	AC015479 Homo sapi
c 45	16.4	86.3	172192	9	AC091921	AC091921 Homo sapi

ALIGNMENTS

RESULT 1
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LOCUS   AX676130   19 bp   DNA   linear   PAT 27-MAR-2003
DEFINITION Sequence 83 from Patent WO02059381.
ACCESSION   AX676130
VERSION   AX676130.1 GI:29333814
KEYWORDS
SOURCE   synthetic construct
  ORGANISM synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Slaugenhaupt,S. and Gusella,J.F.
  TITLE   Gene for identifying individuals with familial dysautonomia
  JOURNAL   Patent: WO 02059381-A 83 01-AUG-2002;
            The General Hospital Corporation (US)
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ORIGIN

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Db   1 CGGATTGTCACTGTTGTGC 19

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LOCUS   BD147310   803 bp   DNA   linear   PAT 17-JAN-2003
DEFINITION Primer for synthesizing full-length cDNA and use thereof.
ACCESSION   BD147310
VERSION   BD147310.1 GI:27853068
KEYWORDS   JP 2002191363-A/2153.
SOURCE   Homo sapiens (human)
  ORGANISM Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

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REFERENCE   1 (bases 1 to 803)
  AUTHORS   Ota,T., Isogai,T., Nishikawa,T., Hayashi,K., Saito,K., Yamamoto,J.,
            Ishii,S., Sugiyama,T., Wakamatsu,A., Nagai,K. and Otsuki,T.
  TITLE     Primer for synthesizing full-length cDNA and use thereof
  JOURNAL   Patent: JP 2002191363-A 2153 09-JUL-2002;
            HELIX RESEARCH INSTITUTE
   SOURCE   Homo sapiens (human)
   OS       Homo sapiens
   PN       JP 2002191363-A/2153
   PD       09-JUL-2002
   PF       28-JUL-2000 JP 2000280990
   PI       Ota,T., Isogai,T., Nishikawa,T., Hayashi,K., Saito,K., Yamamoto,J.,
   PI       SAITO, TOSHIO OTA,TAKAO ISOGAI,TETSUO NISHIKAWA,KOJI HAYASHI,KAORU
   PI       JUNICHI YAMAMOTO,SHIZUKO ISHII,TOMOYASU SUGIYAMA,AI WAKAMATSU,
   PI       KEIICHI NAGAI,TETSUJI OTSUKI
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VERSION     AX867248.1  GI:40021619
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SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
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            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 803)
  AUTHORS   Ota,T., Isogai,T., Nishikawa,T., Hayashi,K., Saito,K., Yamamoto,J.,
            Ishii,S., Sugiyama,T., Wakamatsu,A., Nagai,K. and Otsuki,T.
  TITLE     Primers for synthesizing full-length cDNA and their use
  JOURNAL   Patent: EP 1074617-A 2153 07-FEB-2001;
            Research Association for Biotechnology (JP)
FEATURES    source           Location/Qualifiers
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ORIGIN

Query Match      100.0%;  Score 19;  DB 6;  Length 803;
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Matches 19;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;

Qy          1 CGGATTGTCACTGTTGTGC 19
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Db         78 CGGATTGTCACTGTTGTGC 96
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RESULT 4
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LOCUS       BD157787              2471 bp    DNA     linear   PAT 17-JAN-2003
DEFINITION  Primer for synthesizing full-length cDNA and use thereof.
ACCESSION   BD157787
VERSION     BD157787.1  GI:27863545
KEYWORDS    
SOURCE      Homo sapiens (human)
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REFERENCE   1 (bases 1 to 2471)
  AUTHORS   Ota,T., Isogai,T., Nishikawa,T., Hayashi,K., Saito,K., Yamamoto,J.,
            Ishii,S., Sugiyama,T., Wakamatsu,A., Nagai,K. and Otsuki,T.
  TITLE     Primer for synthesizing full-length cDNA and use thereof
  JOURNAL   Patent: JP 2002191363-A 12630 09-JUL-2002;
            HELIX RESEARCH INSTITUTE
   SOURCE   Homo sapiens (human)
   OS       Homo sapiens
   PN       JP 2002191363-A/12630
   PD       09-JUL-2002
   PF       28-JUL-2000 JP 2000280990
   PI       Ota,T., Isogai,T., Nishikawa,T., Hayashi,K., Saito,K., Yamamoto,J.,
   PI       SAITO, TOSHIO OTA,TAKAO ISOGAI,TETSUO NISHIKAWA,KOJI HAYASHI,KAORU
   PI       JUNICHI YAMAMOTO,SHIZUKO ISHII,TOMOYASU SUGIYAMA,AI WAKAMATSU,
   PI       KEIICHI NAGAI,TETSUJI OTSUKI
   PC       C12N15/09,C07K14/47,C07K16/18,C12N1/15,C12N1/19,C12N1/21,C12N5/ PC
   PC       10,
   PC       C12P21/02,C12Q1/68//C12P21/08,G06F17/30,C12N15/00,C12N5/00 CC
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            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Ota,T., Isogai,T., Nishikawa,T., Hayashi,K., Saito,K., Yamamoto,J.,
            Ishii,S., Sugiyama,T., Wakamatsu,A., Nagai,K. and Otsuki,T.
  TITLE     Primers for synthesizing full-length cDNA and their use
  JOURNAL   Patent: EP 1074617-A 14253 07-FEB-2001;
            Research Association for Biotechnology (JP)
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GenCore version 5.1.6

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Post-processing: Minimum Match 0%
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

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25	15.8	83.2	90583	8	ACD13447	Acd13447 Human DNA
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ALIGNMENTS

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DT   08-NOV-2002  (first entry)
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XX
KW   Human; IKBKAP; Familial Dysautonomia; FD; Riley-Day syndrome;
KW   Hereditary Sensory and Autonomic Neuropathy Type III; carrier screening;
KW   PCR; primer; ss.
XX
OS   Homo sapiens.
XX
XX
XX
PN   WO200259381-A2.
XX
PD   01-AUG-2002.
XX
PF   07-JAN-2002; 2002WO-US0004473.
XX
PR   06-JAN-2001; 2001US-0260080P.
XX
PA   (GEHO ) GEN HOSPITAL CORP.
XX
PI   Slaugenhaupt S, Gusella JF;
XX
DR   WPI; 2002-674806/72.
XX
PT   New IKBKAP genes with mutations, useful for identifying a subject with
PT   familial dysautonomia (FD), or for rapid carrier screening in the
PT   Ashkenazi Jewish population, e.g. screening presymptomatic homozygotes or
PT   prenatal diagnosis.
XX
PS   Claim 33; Page 27; 109pp; English.
XX
CC   The present invention relates to methods and compositions useful for
CC   detecting mutations which cause Familial Dysautonomia (FD, Riley-Day
CC   syndrome, Hereditary Sensory and Autonomic Neuropathy Type III) [OMIM
CC   223900]. It was found that mutations in the IKBKAP gene (see ABQ80565)
CC   are associated with FD. The mutation associated with the major haplotype
CC   of FD, FD1 mutation, is a base pair (bp) mutation, where the thymine
```

CC nucleotide located at bp 6 of intron 20 in the IKBKAP gene is replaced
CC with a cytosine. This results in skipping of exon 20 in the mRNA from FD
CC patients, although they continue to express varying levels of wild-type
CC message in a tissue-specific manner. The mutation associated with the
CC minor haplotype, FD2 mutation, is a bp mutation, where the guanine
CC nucleotide at bp 2397 (bp 73 of exon 19) is replaced with a cytosine.
CC This bp mutation causes an arginine to proline missense mutation (R696P)
CC in the IKBKAP protein, which is predicted to disrupt a potential
CC phosphorylation site. The IKBKAP nucleic acid sequences are useful for
CC identifying a subject with FD and for rapid carrier screening. The IKBKAP
CC gene maps to chromosome 9q31. PCR primers ABQ80558-ABQ80560 were used to
CC detect the splicing defect in IKBKAP gene
XX
SQ Sequence 19 BP; 2 A; 4 C; 6 G; 7 T; 0 U; 0 Other;

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AC AAH05318;
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DT 26-JUN-2001 (first entry)
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KW Human; primer; detection; diagnosis; antisense therapy; gene therapy; ss.
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OS Homo sapiens.
XX
PN EP1074617-A2.
XX
PD 07-FEB-2001.
XX
PF 28-JUL-2000; 2000EP-00116126.
PR 29-JUL-1999; 99JP-00248036.
PR 27-AUG-1999; 99JP-00300253.
PR 11-JAN-2000; 2000JP-00118776.
PR 02-MAY-2000; 2000JP-00183767.
PR 09-JUN-2000; 2000JP-00241899.
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PI Ota T, Isogai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J;
PI Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T;
XX
DR WPI; 2001-318749/34.
XX
PT Primer sets for synthesizing polynucleotides, particularly the 5602 full-
PT length cDNAs defined in the specification, and for the detection and/or
PT diagnosis of the abnormality of the proteins encoded by the full-length
PT cDNAs.
XX
PS Claim 1; SEQ ID NO 2153; 2537pp + Sequence Listing; English.
XX
CC The present invention describes primer sets for synthesizing 5602 full-
CC length cDNAs defined in the specification. Where a primer set comprises:
CC (a) an oligo-dT primer and an oligonucleotide complementary to the
CC complementary strand of a polynucleotide which comprises one of the 5602
CC nucleotide sequences defined in the specification, where the
CC oligonucleotide comprises at least 15 nucleotides; or (b) a combination
CC of an oligonucleotide comprising a sequence complementary to the
CC complementary strand of a polynucleotide which comprises a 5'-end
CC sequence and an oligonucleotide comprising a sequence complementary to a

CC nucleotide located at bp 6 of intron 20 in the IKBKAP gene is replaced

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CC polynucleotide which comprises a 3'-end sequence, where the
CC oligonucleotide comprises at least 15 nucleotides and the combination of
CC the 5'-end sequence/3'-end sequence is selected from those defined in the
CC specification. The primer sets can be used in antisense therapy and in
CC gene therapy. The primers are useful for synthesising polynucleotides,
CC particularly full-length cDNAs. The primers are also useful for the
CC detection and/or diagnosis of the abnormality of the proteins encoded by
CC the full-length cDNAs. The primers allow obtaining of the full-length
CC cDNAs easily without any specialised methods. AAH03166 to AAH13628 and
CC AAH13633 to AAH18742 represent human cDNA sequences; AAB92446 to AAB95893
CC represent human amino acid sequences; and AAH13629 to AAH13632 represent
CC oligonucleotides, all of which are used in the exemplification of the
CC present invention
XX
SQ Sequence 803 BP; 251 A; 154 C; 172 G; 222 T; 0 U; 4 Other;

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AAH15795
AC AAH15795;
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DT 26-JUN-2001 (first entry)
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DE Human cDNA sequence SEQ ID NO:14253.
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KW Human; primer; detection; diagnosis; antisense therapy; gene therapy; ss.
XX
OS Homo sapiens.
XX
PN EP1074617-A2.
XX
PD 07-FEB-2001.
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PF 28-JUL-2000; 2000EP-00116126.
PR 29-JUL-1999; 99JP-00248036.
PR 27-AUG-1999; 99JP-00300253.
PR 11-JAN-2000; 2000JP-00118776.
PR 02-MAY-2000; 2000JP-00183767.
PR 09-JUN-2000; 2000JP-00241899.
XX
PA (HELI;-) HELIX RES INST.
XX
PI Ota T, Isogai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J;
PI Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T;
XX
DR WPI; 2001-318749/34.
XX
PT Primer sets for synthesizing polynucleotides, particularly the 5602 full-
PT length cDNAs defined in the specification, and for the detection and/or
PT diagnosis of the abnormality of the proteins encoded by the full-length
PT cDNAs.
XX
PS Claim 8; SEQ ID NO 14253; 2537pp + Sequence Listing; English.
XX
CC The present invention describes primer sets for synthesizing 5602 full-
CC length cDNAs defined in the specification. Where a primer set comprises:
CC (a) an oligo-dT primer and an oligonucleotide complementary to the
CC complementary strand of a polynucleotide which comprises one of the 5602
CC nucleotide sequences defined in the specification, where the
CC oligonucleotide comprises at least 15 nucleotides; or (b) a combination
CC of an oligonucleotide comprising a sequence complementary to the
CC complementary strand of a polynucleotide which comprises a 5'-end

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Query Match 100.0%; Score 19; DB 6; Length 19;
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                    GenCore version 5.1.6
                    Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

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16	15	78.9	2690	1	US-08-332-643-55	Sequence 55, Appl
17	15	78.9	2690	1	US-08-332-643-61	Sequence 61, Appl
18	15	78.9	3675	4	US-09-107-532A-2566	Sequence 2566, Ap
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c 38	14.8	77.9	880	3	US-09-305-839-7	Sequence 7, Appli
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c 40	14.8	77.9	1320	4	US-09-949-016-1481	Sequence 1481, Ap
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c 43	14.8	77.9	5069	4	US-09-949-016-16120	Sequence 16120, A
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ALIGNMENTS

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; Patent No. 5891719
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;  APPLICANT: Cohen, Lucy
;  APPLICANT: Baeuerle, Patrick
;  TITLE OF INVENTION: IKAP Proteins, Nucleic Acids and Methods
;  NUMBER OF SEQUENCES: 2
;  CORRESPONDENCE ADDRESS:
;   ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
;   STREET: 75 DENISE DRIVE
;   CITY: HILLSBOROUGH
;   STATE: CALIFORNIA
;   COUNTRY: USA
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;   SOFTWARE: PatentIn Release #1.0, Version #1.30
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;   APPLICATION NUMBER: US/08/971,244
;   FILING DATE:
;   CLASSIFICATION: 435
;  ATTORNEY/AGENT INFORMATION:
;   NAME: OSMAN, RICHARD A
;   REGISTRATION NUMBER: 36,627
;   REFERENCE/DOCKET NUMBER: T97-011
;  TELECOMMUNICATION INFORMATION:
;   TELEPHONE: (650) 343-4341
;   TELEFAX: (650) 343-4342
; INFORMATION FOR SEQ ID NO: 1:
;  SEQUENCE CHARACTERISTICS:
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;   TOPOLOGY: linear
;  MOLECULE TYPE: cDNA
;  FEATURE:
;   NAME/KEY: CDS
;   LOCATION: 1..3996
US-08-971-244-1

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Matches   19;  Conservative    0;  Mismatches   0;  Indels    0;  Gaps    0;

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Patent No. 6172195
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;   APPLICANT: Baeuerle, Patrick
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;   NUMBER OF SEQUENCES: 2
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
;   STREET: 75 DENISE DRIVE
;   CITY: HILLSBOROUGH
;   STATE: CALIFORNIA
;   COUNTRY: USA
;   ZIP: 94010
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: PatentIn Release #1.0, Version #1.30
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/09/286,891
;   FILING DATE:
;   CLASSIFICATION:
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: 08/971,244
;   FILING DATE:
;   ATTORNEY/AGENT INFORMATION:
;   NAME: OSMAN, RICHARD A
;   REGISTRATION NUMBER: 36,627
;   REFERENCE/DOCKET NUMBER: T97-011
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE: (650) 343-4342
;   TELEFAX: (650) 343-4341
; INFORMATION FOR SEQ ID NO: 1:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 3999 base pairs
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;   STRANDEDNESS: double
;   TOPOLOGY: linear
;   MOLECULE TYPE: cDNA
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: 1..3996
US-09-286-891-1

Query Match   100.0%; Score 19; DB 3; Length 3999;
Best Local Similarity   100.0%; Pred. No. 2.6;
Matches   19; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   1 CGGATTGTCACTGTGTGC 19
                 ||||||||||||||||||
Db   2086 CGGATTGTCACTGTGTGC 2104

RESULT 3
US-09-270-767-11478/c
Sequence 11478, Application US/09270767
Patent No. 6703491
; GENERAL INFORMATION:
;   APPLICANT: Homburger et al.
;   TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
;   FILE REFERENCE: File Reference: 7326-094
;   CURRENT APPLICATION NUMBER: US/09/270,767
;   CURRENT FILING DATE: 1999-03-17
;   NUMBER OF SEQ ID NOS: 62517
;   SOFTWARE: PatentIn Ver. 2.0
;   SEQ ID NO 11478
;   LENGTH: 1839

; TYPE: DNA
; ORGANISM: Drosophila melanogaster
; FEATURE:
; OTHER INFORMATION: n means any nucleotide
US-09-270-767-11478

Query Match   83.2%; Score 15.8; DB 4; Length 1839;
Best Local Similarity   89.5%; Pred. No. 1.1e+02;
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Qy   1 CGGATTGTCACTGTGTGC 19
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Db   1366 CGGATTGTGACTGTGGTGC 1348

RESULT 4
US-09-602-787A-577
Sequence 577, Application US/09602787A
Patent No. 669561
; GENERAL INFORMATION:
;   APPLICANT: Pompejus, Mark
;   APPLICANT: Kr"ger, Burkhard
;   APPLICANT: Sch"der, Hartwig
;   APPLICANT: Zelder, Oskar
;   APPLICANT: Haberhauer, Gregor
;   TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING PROTEINS
;   TITLE OF INVENTION: INVOLVED IN MEMBRANE SYNTHESIS AND MEMBRANE
;   TITLE OF INVENTION: TRANSPORT
;   FILE REFERENCE: BGI-125CP
;   CURRENT APPLICATION NUMBER: US/09/602,787A
;   CURRENT FILING DATE: 2000-06-23
;   PRIOR APPLICATION NUMBER: USSN 60/141031
;   PRIOR FILING DATE: 1999-06-25
;   PRIOR APPLICATION NUMBER: DE 19931454.3
;   PRIOR FILING DATE: 1999-07-08
;   PRIOR APPLICATION NUMBER: DE 19931478.0
;   PRIOR FILING DATE: 1999-07-08
;   PRIOR APPLICATION NUMBER: DE 19931563.9
;   PRIOR FILING DATE: 1999-07-08
;   PRIOR APPLICATION NUMBER: DE 19932122.1
;   PRIOR FILING DATE: 1999-07-09
;   PRIOR APPLICATION NUMBER: DE 19932124.8
;   PRIOR FILING DATE: 1999-07-09
;   PRIOR APPLICATION NUMBER: DE 19932125.6
;   PRIOR FILING DATE: 1999-07-09
;   PRIOR APPLICATION NUMBER: DE 19932128.0
;   PRIOR FILING DATE: 1999-07-09
;   PRIOR APPLICATION NUMBER: DE 19932180.9
;   PRIOR FILING DATE: 1999-07-09
;   PRIOR APPLICATION NUMBER: DE 19932182.5
;   PRIOR FILING DATE: 1999-07-09
;   PRIOR APPLICATION NUMBER: DE 19932183.3
;   PRIOR FILING DATE: 1999-07-09
;   PRIOR APPLICATION NUMBER: DE 19932190.6
;   PRIOR FILING DATE: 1999-07-09
;   PRIOR APPLICATION NUMBER: DE 19932191.4
;   PRIOR FILING DATE: 1999-07-09
;   PRIOR APPLICATION NUMBER: DE 19932209.0
;   PRIOR FILING DATE: 1999-07-09
;   PRIOR APPLICATION NUMBER: DE 19932212.0
;   PRIOR FILING DATE: 1999-07-09
;   PRIOR APPLICATION NUMBER: DE 19932227.9
;   PRIOR FILING DATE: 1999-07-09
;   PRIOR APPLICATION NUMBER: DE 19932228.7
;   PRIOR FILING DATE: 1999-07-09
;   PRIOR APPLICATION NUMBER: DE 19932229.5
;   PRIOR FILING DATE: 1999-07-09
;   PRIOR APPLICATION NUMBER: DE 19932230.9
;   PRIOR FILING DATE: 1999-07-09
;   PRIOR APPLICATION NUMBER: DE 19932927.3
;   PRIOR FILING DATE: 1999-07-14
;   PRIOR APPLICATION NUMBER: DE 19933005.0
;   PRIOR FILING DATE: 1999-07-14
;   PRIOR APPLICATION NUMBER: DE 19933006.9
;   PRIOR FILING DATE: 1999-07-14

OM nucleic - nucleic search, using sw model

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GenCore version 5.1.6

Run on: July 31, 2005, 16:38:33 ; Search time 193.988 Seconds
            (without alignments)
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Title: US-10-041-856-83
Perfect score: 19
Sequence: 1 cggattgtcacgttgtgc 19

Scoring table: IDENTITY_NUC
                Gapop 10.0 , Gapext 1.0

Searched: 7287783 seqs, 3236178273 residues

Total number of hits satisfying chosen parameters: 14575566

Post-processing: Minimum Match 0%
Maximum DB seq length: 0
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Maximum Match 100%
Listing first 45 summaries

Database : Published Applications NA:*

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24: /cgn2_6/ptcodata/1/pubpna/US10_NEW_PUB.seq:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	19	100.0	19	13	US-10-041-856-83	Sequence 83, Appl
2	19	100.0	4803	10	US-10-719-993-4585	Sequence 276, App
3	19	100.0	4803	21	US-10-956-213-276	Sequence 276, Ap
4	19	100.0	5924	13	US-10-956-157-1094	Sequence 1094, Ap
5	19	100.0	6479	13	US-10-041-856-2	Sequence 2, Appli
6	18.6	97.9	201	13	US-10-041-856-1	Sequence 1, Appli
7	18.6	97.9	201	20	US-10-719-993-4499	Sequence 4499, Ap
					US-10-719-993-4527	Sequence 4527, Ap
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 8: 18.6 97.9 201   US-10-719-993-4556 Sequence 4556, Ap
 9: 18.6 97.9 201   US-10-719-993-4585 Sequence 4585, Ap
10: 18.6 97.9 201   US-10-719-993-4613 Sequence 4613, Ap
11: 18.6 97.9 201   US-10-719-993-34995 Sequence 34995, A
12: 18.6 97.9 201   US-10-719-993-319 Sequence 319, App
13: 18.6 97.9 201   US-10-719-993-322 Sequence 322, App
14: 18.6 97.9 201   US-10-719-993-320 Sequence 320, App
15: 18.6 97.9 201   US-10-719-993-321 Sequence 321, App
16: 18.6 97.9 201   US-10-719-993-318 Sequence 318, App
17: 18.6 97.9 201   US-10-719-993-6863 Sequence 6863, Ap
18: 17.4 91.6 21    US-10-913-280-548 Sequence 548, App
19: 18 94.7 19      US-10-913-280-549 Sequence 549, App
20: 17 89.5 18      US-10-913-280-123 Sequence 123, App
21: 16 84.2 22      US-10-972-079-73099 Sequence 73099, A
22: 16 84.2 21      US-10-972-079-1312 Sequence 1312, Ap
23: 15.8 83.2 412   US-10-767-701-1312 Sequence 20615, A
24: 15.8 83.2 2544  US-10-972-079-20615 Sequence 577, App
25: 15.8 83.2 2733  US-09-738-626-1 Sequence 1, Appli
26: 15.8 83.2 3305400 US-09-738-626-488 Sequence 488, App
27: 15.4 81.1 408   US-10-027-632-1 Sequence 75776, A
28: 15.4 81.1 474   US-10-425-115-75776 Sequence 3993, Ap
29: 15.4 81.1 474   US-10-027-632-3993 Sequence 3994, Ap
30: 15.4 81.1 474   US-10-027-632-3994 Sequence 3995, Ap
31: 15.4 81.1 474   US-10-027-632-3993 Sequence 3993, Ap
32: 15.4 81.1 474   US-10-027-632-3995 Sequence 3994, Ap
33: 15.4 81.1 474   US-10-027-632-3994 Sequence 3995, Ap
34: 15.4 81.1 592   US-10-021-323-15066 Sequence 15066, A
35: 15.4 81.1 638   US-10-425-114-35933 Sequence 35933, A
36: 15.4 81.1 749   US-10-437-963-56184 Sequence 56184, A
37: 15.4 81.1 1067  US-10-767-795-2976 Sequence 2976, Ap
38: 15.4 81.1 1800  US-09-974-300-1667 Sequence 1667, Ap
39: 15.4 81.1 2682  US-10-282-122A-38266 Sequence 38266, A
40: 15.4 81.1 2694  US-10-425-114-31968 Sequence 31968, A
41: 15.4 81.1 2804  US-10-425-115-20896 Sequence 20896, A
42: 15.4 81.1 2976  US-10-425-115-1163362 Sequence 1163362,
43: 15.4 81.1 3350  US-10-152-319A-2081 Sequence 2081, Ap
44: 15.4 81.1 5961  US-10-429-802-35 Sequence 35, Appl
45: 15.4 81.1 5961  US-10-430-503-26 Sequence 26, Appl
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ALIGNMENTS

RESULT 1
US-10-041-856-83

; Sequence 83, Application US/10041856
; Publication No. US20020169299A1
; GENERAL INFORMATION:
; APPLICANT: SLAUGENHAUPT, SUSAN
; APPLICANT: GUSELLA, JAMES F.
; TITLE OF INVENTION: GENE FOR IDENTIFYING INDIVIDUALS WITH FAMILIAL
; TITLE OF INVENTION: DYSAUTONOMIA
; FILE REFERENCE: 1829-4004US1
; CURRENT APPLICATION NUMBER: US/10/041,856
; CURRENT FILING DATE: 2002-07-08
; PRIOR APPLICATION NUMBER: 60/260,080
; PRIOR FILING DATE: 2001-01-06
; NUMBER OF SEQ ID NOS: 88
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 83
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer
US-10-041-856-83

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Best Local Similarity   100.0%; Pred. No. 5.3;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy   1 CGGATTGTCACTGTTGTGC 19
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Db   1 CGGATTGTCACTGTGTGC 19

RESULT 2
US-09-930-213-276
; Sequence 276, Application US/09930213
; Publication No. US20030170625A1
; GENERAL INFORMATION:
;   APPLICANT: ROSENTHAL, ANDRE
;   APPLICANT: HINZMANN, BERND
;   APPLICANT: SCHAFER, REINHARD
;   APPLICANT: ZUBER, JOHANNES
;   APPLICANT: TCHE-NITSE, OLEG
;   APPLICANT: GRIPS, MARTIN
;   APPLICANT: HELLNEGEL, MARTIN
;   APPLICANT: SCHMITZ, ANNE-CHANTAL
;   APPLICANT: SERS, CHRISTINE
;   TITLE OF INVENTION: DETECTION OF DIFFERENTIAL GENE EXPRESSIONS
;   FILE REFERENCE: ALBRE-14
;   CURRENT APPLICATION NUMBER: US/09/930,213
;   CURRENT FILING DATE: 2001-01-31
;   PRIOR APPLICATION NUMBER: DE 10004102.7
;   PRIOR FILING DATE: 2000-01-31
;   NUMBER OF SEQ ID NOS: 885
;   SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 276
;   LENGTH: 4803
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-930-213-276

Qy   Query Match   100.0%; Score 19; DB 10; Length 4803;
        Best Local Similarity   100.0%; Pred. No. 10;
        Matches   19; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   1 CGGATTGTCACTGTGTGC 19
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Db   2389 CGGATTGTCACTGTGTGC 2407

RESULT 3
US-10-956-157-1094
; Sequence 1094, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
;   APPLICANT: Wyeth
;   APPLICANT: Mounts, William
;   TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
;   FILE REFERENCE: 031896-043000 (AM 101081)
;   CURRENT APPLICATION NUMBER: US/10/956,157
;   CURRENT FILING DATE: 2004-10-04
;   NUMBER OF SEQ ID NOS: 319805
;   SOFTWARE: Patentin version 3.2
; SEQ ID NO 1094
;   LENGTH: 4803
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-956-157-1094

        Query Match   100.0%; Score 19; DB 21; Length 4803;
        Best Local Similarity   100.0%; Pred. No. 10;
        Matches   19; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   1 CGGATTGTCACTGTGTGC 19
              ||||||||||||||||||
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RESULT 4
US-10-041-856-2
; Sequence 2, Application US/10041856
; Publication No. US20020169299A1

; GENERAL INFORMATION:
;   APPLICANT: SLAUGENHAUPT, SUSAN
;   APPLICANT: GUSELLA, JAMES F.
;   TITLE OF INVENTION: GENE FOR IDENTIFYING INDIVIDUALS WITH FAMILIAL
;   TITLE OF INVENTION: DYSAUTONOMIA
;   FILE REFERENCE: 1829-4004US1
;   CURRENT APPLICATION NUMBER: US/10/041,856
;   CURRENT FILING DATE: 2002-07-08
;   PRIOR APPLICATION NUMBER: 60/260,080
;   PRIOR FILING DATE: 2001-01-06
;   NUMBER OF SEQ ID NOS: 88
;   SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 2
;   LENGTH: 5924
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-041-856-2

Qy   Query Match   100.0%; Score 19; DB 13; Length 5924;
        Best Local Similarity   100.0%; Pred. No. 10;
        Matches   19; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   1 CGGATTGTCACTGTGTGC 19
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Db   2396 CGGATTGTCACTGTGTGC 2414

RESULT 5
US-10-041-856-1
; Sequence 1, Application US/10041856
; Publication No. US20020169299A1
; GENERAL INFORMATION:
;   APPLICANT: SLAUGENHAUPT, SUSAN
;   APPLICANT: GUSELLA, JAMES F.
;   TITLE OF INVENTION: GENE FOR IDENTIFYING INDIVIDUALS WITH FAMILIAL
;   TITLE OF INVENTION: DYSAUTONOMIA
;   FILE REFERENCE: 1829-4004US1
;   CURRENT APPLICATION NUMBER: US/10/041,856
;   CURRENT FILING DATE: 2002-07-08
;   PRIOR APPLICATION NUMBER: 60/260,080
;   PRIOR FILING DATE: 2001-01-06
;   NUMBER OF SEQ ID NOS: 88
;   SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 1
;   LENGTH: 66479
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-041-856-1

Qy   Query Match   100.0%; Score 19; DB 13; Length 66479;
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Qy   1 CGGATTGTCACTGTGTGC 19
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Db   33713 CGGATTGTCACTGTGTGC 33731

RESULT 6
US-10-719-993-4499
; Sequence 4499, Application US/10719993
; Publication No. US20040265849A1
; GENERAL INFORMATION:
;   APPLICANT: CARGILL, Michele et al.
;   TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
;   TITLE OF INVENTION: ALZHEIMER'S DISEASE, METHODS OF DETECTION AND USES THEREOF
;   FILE REFERENCE: CL001496
;   CURRENT APPLICATION NUMBER: US/10/719,993
;   CURRENT FILING DATE: 2003-11-24
;   NUMBER OF SEQ ID NOS: 55342
;   SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 4499
;   LENGTH: 201

OM nucleic - nucleic search, using sw model

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Title:             US-10-041-856-83
Perfect score:     19
Sequence:          1 cggatgtgcactgttgtgc 19
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Searched:          34239544 seqs, 1903213470D residues
Total number of hits satisfying chosen parameters:     68479088

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
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                   8: gb_gss1:*
                   9: gb_gss2:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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  7     19    100.0   618     4  BG395601   BG395601 602458222
  8     19    100.0   641     5  BQ007986   BQ007986 NISC_kk12
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 16     19    100.0  3833     7  CR749385   CR749385 ILLUMIGEN
 17     19    100.0  3999     9  AY414501   AY414501 Homo sapi
 18     19    100.0  3999     9  AY414502   AY414502 Pan trogl
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 20     17    89.5   625      9  CE786192   CE786192 tigr-gss-
c 21    17    89.5   703      4  BM657393   BM657393 170006874
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 23     16.4  86.3   425      2  BE495948   BE495948 WHE1259_A
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 25     16.4  86.3   470      9  CL571732   CL571732 OB_Ba001
 26     16.4  86.3   501      2  BE586622   BE586622 WHE0509_E
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 28     16.4  86.3   521      1  AU248858   AU248858 AU248858
 29     16.4  86.3   542      4  BI728641   BI728641 103110E0
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c 32    16.4  86.3   577      4  BU280892   BU280892 BU280892
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c 34    16.4  86.3   591      5  BU991273   BU991273 HD06H05r
 35     16.4  86.3   613      4  BM002833   BM002833 103110B6
 36     16.4  86.3   614      4  BI995634   BI995634 103102B6
 37     16.4  86.3   628      5  CA632741   CA632741 wlein.pk0
 38     16.4  86.3   631      6  CD876595   CD876595 AZ03.1110E
 39     16.4  86.3   636      4  BJ287535   BJ287535 BJ287535
 40     16.4  86.3   649      6  CD917401   CD917401 G608.11D5D
c 41    16.4  86.3   660      5  BQ238523   BQ238523 TaE05003B
c 42    16.4  86.3   666      9  CE628574   CE628574 tigr-gss-
c 43    16.4  86.3   666      1  AL646873   AL646873 103110100
c 44    16.4  86.3   668      4  BM002132   BM002132 103110E0D
c 45    16.4  86.3   672      8  BZ745940   BZ745940 QGBEN94TM
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ALIGNMENTS

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ACCESSION   CN256146
VERSION     CN256146.1  GI:47272560
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 417)
  AUTHORS   Brandenberger,R., Wei,H., Zhang,S., Lei,S., Murage,J., Fisk,G.J.,
            Li,Y., Xu,C., Fang,R., Guegler,K., Rao,M.S., Mandalam,R.,
            Lebkowski,J and Stanton,L.W.
  TITLE     Transcriptome characterization elucidates signaling networks that
            control human ES cell growth and differentiation
  JOURNAL   Nat. Biotechnol. 22 (6), 707-716 (2004)
COMMENT     Contact: Brandenberger R
            Regenerative Medicine
            Geron Corporation
            230 Constitution Drive, Menlo Park, CA 94025, USA
            Tel: 650 473 8658
            Fax: 650 473 7760
            Email: rbrandenberger@geron.com
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                     H9"
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                     and H9 (p26) maintained in feeder-free conditions"
ORIGIN

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RESULT 2
LOCUS   BF840993/c
DEFINITION   RC3-HT0974-011200-013-a03 HT0974 Homo sapiens cDNA, mRNA sequence.
ACCESSION   BF840993
VERSION   BF840993.1 GI:1219364l
KEYWORDS   EST.
SOURCE   Homo sapiens (human)
ORGANISM   Homo sapiens
                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 447)
AUTHORS   Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
                Nagai,M.A., da Silva,W.Jr., Zago,M.A., Bordin,S., Costa,F.F.,
                Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
                Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., and
                O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
                Simpson,A.J.
TITLE   Shotgun sequencing of the human transcriptome with ORF expressed
                sequence tags
JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
MEDLINE   20202663
PUBMED   10737800
COMMENT   Contact: Simpson A.J.G.
                Laboratory of Cancer Genetics
                Ludwig Institute for Cancer Research
                Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                Brazil
                Tel: +55-11-2704922
                Fax: +55-11-2707001
                Email: asimpson@ludwig.org.br
                This sequence was derived from the FAPESP/LICR Human Cancer Genome
                Project.
                (http://www.ludwig.org.br/scripts/gethtml2.pl?ti=RC3&t2=HT0974-
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                     Site 2: SmaI; A mini-library was made by cloning products
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Best Local Similarity   100.0%;
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RESULT 3
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DEFINITION   DKFZp686G02155_r1 686 (synonym: hlcc3) Homo sapiens cDNA clone
                DKFZp686G02155 5', mRNA sequence.
ACCESSION   AL702133
VERSION   AL702133.1 GI:19685488
KEYWORDS   EST.
SOURCE   Homo sapiens (human)

ORGANISM   Homo sapiens
                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 513)
AUTHORS   Bloecker,H., Boecher,M., Brandt,P., Mewes,W., Weil,B. and
                Wiemann,S.
TITLE   EST (Bloecker,H., Boecher,M., Brandt,P., Mewes,H.W., Weil,B. and
                Wiemann,S.)
JOURNAL   Unpublished (1999)
COMMENT   Contact: MIPS
                MIPS
                Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany
                This is the 5' sequence of the clone insert
                Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
                Research Center (DKFZ); Email B.wiemann@dkfz-heidelberg.de;
                sequenced by GBF (National Research Centre for Biotechnology Ltd.,
                Braunschweig/Germany) within the cDNA sequencing consortium of the
                German Genome Project.
                No sl sequence available.
                This clone (DKFZp686G02155) is available at the RZPD in Berlin.
                Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
                Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.
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Query Match   100.0%; Score 19; DB 1; Length 513;
Best Local Similarity   100.0%;
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RESULT 4
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DEFINITION   ij77dll.x1 Human insulinoma Homo sapiens cDNA clone IMAGE:5636805
                3' similar to SW:IKI3_YEAST Q06706 IKI3 PROTEIN. ;, mRNA sequence.
ACCESSION   BM512007
VERSION   BM512007.1 GI:18683150
KEYWORDS   EST.
SOURCE   Homo sapiens (human)
ORGANISM   Homo sapiens
                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 553)
AUTHORS   Melton,D., Brown,J., Kenty,G., Permutt,A., Lee,C., Kaestner,K.,
                Lemishka,I., Scearce,M., Brestelli,J., Gradwohl,G., Clifton,S.,
                Hillier,L., Marra,M., Pape,D., Wylie,T., Martin,J., Blistein,A.,
                Schmitt,A., Theising,B., Ritter,E., Ronko,I., Bennett,J.,
                Cardenas,M., Gibbons,M., McCann,R., Cole,R., Tsagareishvili,R.,
                Williams,T., Jackson,Y. and Bowers,Y.
TITLE   Endocrine Pancreas Consortium
JOURNAL   Unpublished (2000)
COMMENT   Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
                Endocrine Pancreas Consortium
                Harvard University, Howard Hughes Medical Institute
                Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,
                MA 02138
                Tel: 617-495-1812
                Fax: 617-495-8557
                Email: dmelton@biohp.harvard.edu

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OM nucleic - nucleic search, using sw model

Run on: July 31, 2005, 14:44:02 ; Search time 575.679 Seconds
                                            (without alignments)
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Scoring table: IDENTITY_NUC
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Searched: 4708233 seqs, 2422607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

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SUMMARIES

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3	20	100.0	803	6	AX867248	AX867248 Sequence
4	20	100.0	828	6	BD147338	BD147338 Primer fo
5	20	100.0	828	6	AX867276	AX867276 Sequence
6	20	100.0	2471	6	BD157787	BD157787 Primer fo
7	20	100.0	2471	6	AX879348	AX879348 Sequence
8	20	100.0	2471	6	AK022559	AK022559 Homo sapi
9	20	100.0	2712	6	BD160487	BD160487 Primer fo
10	20	100.0	2712	6	AX883713	AX883713 Sequence
11	20	100.0	2712	6	AK024223	AK024223 Homo sapi
12	20	100.0	3516	6	CQ724004	CQ724004 Sequence
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14	20	100.0	3999	6	AR124807	AR124807 Sequence
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18	20	100.0	4788	6	AX877177	AX877177 Sequence
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21	20	100.0	4803	6	BD173600	BD173600 Method of
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33	16.8	84.0	113715	2	AC149149	AC149149 Xenopus t
34	16.8	84.0	116557	9	AC107022	AC107022 Homo sapi
35	16.8	84.0	132642	2	AC164404	AC164404 Pan trogl
36	16.8	84.0	136547	2	AC134966	AC134966 Gallus ga
37	16.8	84.0	149335	2	AC009651	AC009651 Homo sapi
38	16.8	84.0	174028	2	AC067831	AC067831 Homo sapi
39	16.8	84.0	180389	9	AC063944	AC063944 Homo sapi
40	16.8	84.0	195265	9	AC012071	AC012071 Homo sapi
41	16.8	84.0	199390	3	AC091501	AC091501 Drosophil
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43	16.8	84.0	228998	2	AC112472	AC112472 Rattus no
44	16.8	84.0	231264	2	AC095739	AC095739 Rattus no
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

ALIGNMENTS

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LOCUS   AX676131   20 bp   DNA   linear   PAT 27-MAR-2003
DEFINITION   Sequence 84 from Patent WO02059381.
ACCESSION   AX676131
VERSION   AX676131.1 GI:29333815
KEYWORDS   .
SOURCE   synthetic construct
  ORGANISM   synthetic construct
                other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Slaugenhaupt,S. and Gusella,J.F.
  TITLE   Gene for identifying individuals with familial dysautonomia
  JOURNAL   Patent: WO 02059381-A 84 01-AUG-2002;
                The General Hospital Corporation (US)
FEATURES   Location/Qualifiers
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LOCUS   BD147310   803 bp   DNA   linear   PAT 17-JAN-2003
DEFINITION   Primer for synthesizing full-length cDNA and use thereof.
ACCESSION   BD147310
VERSION   BD147310.1 GI:27853068
KEYWORDS   JP 2002191363-A/2163.
SOURCE   Homo sapiens (human)
  ORGANISM   Homo sapiens
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RESULT 3

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LOCUS       AX867248                          803 bp    DNA     linear   PAT 17-DEC-2003
DEFINITION  Sequence 2153 from Patent EP1074617.
ACCESSION   AX867248
VERSION     AX867248.1  GI:40021619
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 803)
  AUTHORS   Ota,T., Isogai,T., Nishikawa,T., Hayashi,K., Saito,K., Yamamoto,J.,
            Ishii,S., Sugiyama,T., Wakamatsu,A., Nagai,K. and Otsuki,T.
  TITLE     Primers for synthesizing full-length cDNA and their use
  JOURNAL   Patent: EP 1074617-A 2153 07-FEB-2001;
            Research Association for Biotechnology (JP)
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DEFINITION  Primer for synthesizing full-length cDNA and use thereof.
ACCESSION   BD147338
VERSION     BD147338.1  GI:27853096
KEYWORDS    JP 2002191363-A/2181.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 828)
  AUTHORS   Ota,T., Isogai,T., Nishikawa,T., Hayashi,K., Saito,K., Yamamoto,J.,
            Ishii,S., Sugiyama,T., Wakamatsu,A., Nagai,K. and Otsuki,T.
  TITLE     Primer for synthesizing full-length cDNA and use thereof
  JOURNAL   Patent: JP 2002191363-A 2181 09-JUL-2002;
            HELIX RESEARCH INSTITUTE
COMMENT     OS   Homo sapiens (human)
            PN   JP 2002191363-A/2181
            PD   09-JUL-2002
            PF   28-JUL-2000 JP 2000280990
            PI   TOSHIO OTA,TAKAO ISOGAI,TETSUO NISHIKAWA,KOJI HAYASHI,KAORU
            PI   SAITO,
            PI   JUNICHI YAMAMOTO,SHIZUKO ISHII,TOMOYASU SUGIYAMA,AI WAKAMATSU,
            PI   KEIICHI NAGAI,TETSUJI OTSUKI
            PC   C12N15/09,C07K14/47,C07K16/18,C12N1/15,C12N1/19,C12N1/21,C12N5/ PC
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ORIGIN

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RESULT 5

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ACCESSION   AX867276
VERSION     AX867276.1  GI:40021656
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
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            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 828)
  AUTHORS   Ota,T., Isogai,T., Nishikawa,T., Hayashi,K., Saito,K., Yamamoto,J.,
            Ishii,S., Sugiyama,T., Wakamatsu,A., Nagai,K. and Otsuki,T.
  TITLE     Primers for synthesizing full-length cDNA and their use
  JOURNAL   Patent: EP 1074617-A 2181 07-FEB-2001;
            Research Association for Biotechnology (JP)
FEATURES             Location/Qualifiers
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ACCESSION   BD147338
VERSION     BD147338.1  GI:27853096
KEYWORDS    JP 2002191363-A/2181.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
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            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 828)
  AUTHORS   Ota,T., Isogai,T., Nishikawa,T., Hayashi,K., Saito,K., Yamamoto,J.,
            Ishii,S., Sugiyama,T., Wakamatsu,A., Nagai,K. and Otsuki,T.
  TITLE     Primer for synthesizing full-length cDNA and use thereof
  JOURNAL   Patent: JP 2002191363-A 2181 09-JUL-2002;
            HELIX RESEARCH INSTITUTE
COMMENT     OS   Homo sapiens (human)
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            PF   28-JUL-2000 JP 2000280990
            PI   TOSHIO OTA,TAKAO ISOGAI,TETSUO NISHIKAWA,KOJI HAYASHI,KAORU
            PI   SAITO,
            PI   JUNICHI YAMAMOTO,SHIZUKO ISHII,TOMOYASU SUGIYAMA,AI WAKAMATSU,
            PI   KEIICHI NAGAI,TETSUJI OTSUKI
            PC   C12N15/09,C07K14/47,C07K16/18,C12N1/15,C12N1/19,C12N1/21,C12N5/ PC
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
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3	20	100.0	828	4	AAH05346	Aah05346 Human CDN
4	20	100.0	2471	4	AAH15795	Aah15795 Human cDN
5	20	100.0	2712	4	AAH18495	Aah18495 Human CDN
6	20	100.0	3999	2	AAX28025	Aax28025 Human IKA
7	20	100.0	3999	4	AAF29756	Aaf29756 Human IKA
8	20	100.0	4417	13	ADR07102	Adr07102 Full leng
9	20	100.0	4788	4	AAH14533	Aah14533 Human cDN
10	20	100.0	4803	5	AAH81767	Aah81767 Human dif
11	20	100.0	4803	6	AAL44190	Aal44190 Human I-k
12	20	100.0	5924	6	ABQ80570	Abq80570 Mutant hu
13	20	100.0	5924	6	ABQ80569	Abq80569 Human IKB
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15	20	100.0	6479	6	ABQ80567	Abq80567 Mutant hu
16	20	100.0	6479	6	ABQ80566	Abq80566 Mutant hu
17	20	100.0	6479	6	ABQ80568	Abq80568 Mutant hu
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22	15.8	79.0	405	6	ABT01424	Abt01424 Human neu
23	15.8	79.0	405	6	ABT02917	Abt02917 Human neu
24	15.8	79.0	405	12	ADH77679	Adh77679 Human neu
25	15.8	79.0	621	13	ADQ52747	Adq52747 Novel can
26	15.8	79.0	1035	12	ADK16160	Adk16160 Nanoarcha
27	15.8	79.0	1035	12	AAD46552	Aad46552 Human cMO
28	15.8	79.0	29844	11	ACN45162	Acn45162 Human gen
29	15.8	79.0	51615	4	AAK95240_09	Aak95240_09 Nanoarcha
30	15.8	79.0	110000	4	AAK96713_09	Aak96713_09 Human can
31	15.8	79.0	110000	6	ABT00010_09	Abt00010_09 Human neu
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33	15.8	79.0	110000	12	ADH77486_09	Adh77486_09 Continuation (10 o
34	15.8	79.0	110000	12	ADK16049_0	Adk16049_0 Continuation (10 o
35	15.8	79.0	180227	13	ADD33268	Abd33268 Human can
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37	15.4	77.0	527	10	ADB51555	Adb51555 Primary r
38	15.4	77.0	637	13	ACA27727	Aca27727 Prokaryot
39	15.4	77.0	702	8	ACA27620	Aca27620 Prokaryot
40	15.4	77.0	1350	8	AB214834	Abz14834 Arabidops
41	15.4	77.0	1602	6	ADA68575	Ada68575 Arabidops
42	15.4	77.0	1602	8	ABQ94264	Abq94264 lovP gene
43	15.4	77.0	2550	6	ABN79909	Abn79909 Fungal ZB
44	15.4	77.0	5436	2	AAV72895	Aav72895 Mouse UCP
45	15.4	77.0	5436	3	AAZ24193	Aaz24193 Mouse UCP

ALIGNMENTS

RESULT 1
ABQ80560
ID ABQ80560 standard; DNA; 20 BP.
XX
AC ABQ80560;
XX
DT 08-NOV-2002 (first entry)
XX
DE IKBKAP PCR primer 23R.
XX
KW Human; IKBKAP; Familial Dysautonomia; FD; Riley-Day syndrome;
KW Hereditary Sensory and Autonomic Neuropathy Type III; carrier screening;
KW PCR; primer; ss.
XX
OS Homo sapiens.
XX
PN WO020025938l-A2.
XX
PD 01-AUG-2002.
XX
PF 07-JAN-2002; 2002WO-US000473.
XX
PR 06-JAN-2001; 2001US-0260080P.
XX
PA (GEHO) GEN HOSPITAL CORP.
XX
PI Slaugenhaupt S, Gusella JF;
XX
DR WPI; 2002-674806/72.
XX
PT New IKBKAP genes with mutations, useful for identifying a subject with
PT familial dysautonomia (FD), or for rapid carrier screening in the
PT Ashkenazi Jewish population, e.g. screening presymptomatic homozygotes or
PT prenatal diagnosis.
XX
PS Claim 33; Page 27; 109pp; English.
XX
CC The present invention relates to methods and compositions useful for
CC detecting mutations which cause Familial Dysautonomia (FD, Riley-Day
CC syndrome, Hereditary Sensory and Autonomic Neuropathy Type III) [OMIM
CC 223900]. It was found that mutations in the IKBKAP gene (see ABQ80565)
CC are associated with FD. That the mutation associated with the major haplotype
CC of FD, FD1 mutation, is a base pair (bp) mutation, where the thymine

CC   nucleotide located at bp 6 of intron 20 in the IKBKAP gene is replaced
CC   with a cytosine. This results in skipping of exon 20 in the mRNA from FD
CC   patients, although they continue to express varying levels of wild-type
CC   message in a tissue-specific manner. The mutation associated with the
CC   minor haplotype, FD2 mutation, is a bp mutation, where the guanine
CC   nucleotide at bp 2397 (bp 73 of exon 19) is replaced with a cytosine.
CC   This bp mutation causes an arginine to proline missense mutation (R696P)
CC   in the IKBKAP protein, which is predicted to disrupt a potential
CC   phosphorylation site. The IKBKAP nucleic acid sequences are useful for
CC   identifying a subject with FD and for rapid carrier screening. The IKBKAP
CC   gene maps to chromosome 9q31. PCR primers ABQ80558-ABQ80560 were used to
CC   detect the splicing defect in IKBKAP gene
XX
SQ   Sequence 20 BP; 4 A; 7 C; 4 G; 5 T; 0 U; 0 Other;

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Query Match             100.0%;  Score 20;  DB 6;  Length 20;
Best Local Similarity   100.0%;  Pred. No. 1.6;
Matches    20;          Conservative   0;  Mismatches   0;  Indels   0;  Gaps   0;

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Db          1 GACTGCTCTCATAGCATCGC 20
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RESULT 2

AAH05318/c

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AC   AAH05318;
XX
DT   26-JUN-2001 (first entry)
XX
DE   Human cDNA clone (5'-primer) SEQ ID NO:2153.
XX
KW   Human; primer; detection; diagnosis; antisense therapy; gene therapy; ss.
XX
OS   Homo sapiens.
XX
PN   EP1074617-A2.
XX
PD   07-FEB-2001.
XX
PF   28-JUL-2000; 2000EP-00116126.
XX
PR   29-JUL-1999;   99JP-00248036.
PR   27-AUG-1999;   99JP-00300253.
PR   11-JAN-2000;   2000JP-00118776.
PR   02-MAY-2000;   2000JP-00183767.
PR   09-JUN-2000;   2000JP-00241899.
XX
PA   (HELI-) HELIX RES INST.
XX
PI   Ota T, Isogai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J;
PI   Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T;
XX
DR   WPI; 2001-318749/34.
XX
PT   Primer sets for synthesising polynucleotides, particularly the 5602 full-
PT   length cDNAs defined in the specification, and for the detection and/or
PT   diagnosis of the abnormality of the proteins encoded by the full-length
PT   cDNAs.
XX
PS   Claim 1; SEQ ID NO 2153; 2537pp + Sequence Listing; English.
XX
CC   The present invention describes primer sets for synthesising 5602 full-
CC   length cDNAs defined in the specification. Where a primer set comprises:
CC   (a) an oligo-dT primer and an oligonucleotide complementary to the
CC   complementary strand of a polynucleotide which comprises one of the 5602
CC   nucleotide sequences defined in the specification, where the
CC   oligonucleotide comprises at least 15 nucleotides; or (b) a combination
CC   of an oligonucleotide comprising a sequence complementary to the
CC   complementary strand of a polynucleotide comprising a sequence
CC   complementary to a 5'-end
CC   sequence and an oligonucleotide comprising a sequence complementary to a
CC   polynucleotide which comprises a 3'-end sequence, where the
CC   oligonucleotide comprises at least 15 nucleotides and the combination of
CC   the 5'-end sequence/3'-end sequence is selected from those defined in the
CC   specification. The primer sets can be used in antisense therapy and in
CC   gene therapy. The primer sets are useful for synthesising polynucleotides,
CC   particularly full-length cDNAs. The primers are also useful for the
CC   detection and/or diagnosis of the abnormality of the proteins encoded by
CC   the full-length cDNAs. The primers allow obtaining of the full-length
CC   cDNAs easily without any specialised methods. AAH03166 to AAH13628 and
CC   AAH13633 to AAH18742 represent human cDNA sequences; AAB92446 to AAB95893
CC   represent human amino acid sequences; and AAH13629 to AAH13632 represent
CC   oligonucleotides, all of which are used in the exemplification of the
CC   present invention
XX
SQ   Sequence 803 BP; 251 A; 154 C; 172 G; 222 T; 0 U; 4 Other;

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Query Match             100.0%;  Score 20;  DB 4;  Length 803;
Best Local Similarity   100.0%;  Pred. No. 2.5;
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ID   AAH05346 standard; cDNA; 828 BP.
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AC   AAH05346;
XX
DT   26-JUN-2001 (first entry)
XX
DE   Human cDNA clone (5'-primer) SEQ ID NO:2181.
XX
KW   Human; primer; detection; diagnosis; antisense therapy; gene therapy; ss.
XX
OS   Homo sapiens.
XX
PN   EP1074617-A2.
XX
PD   07-FEB-2001.
XX
PF   28-JUL-2000; 2000EP-00116126.
XX
PR   29-JUL-1999;   99JP-00248036.
PR   27-AUG-1999;   99JP-00300253.
PR   11-JAN-2000;   2000JP-00118776.
PR   02-MAY-2000;   2000JP-00183767.
PR   09-JUN-2000;   2000JP-00241899.
XX
PA   (HELI-) HELIX RES INST.
XX
PI   Ota T, Isogai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J;
PI   Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T;
XX
DR   WPI; 2001-318749/34.
XX
PT   Primer sets for synthesising polynucleotides, particularly the 5602 full-
PT   length cDNAs defined in the specification, and for the detection and/or
PT   diagnosis of the abnormality of the proteins encoded by the full-length
PT   cDNAs.
XX
PS   Claim 1; SEQ ID NO 2181; 2537pp + Sequence Listing; English.
XX
CC   The present invention describes primer sets for synthesising 5602 full-
CC   length cDNAs defined in the specification. Where a primer set comprises:
CC   (a) an oligo-dT primer and an oligonucleotide complementary to the
CC   complementary strand of a polynucleotide which comprises one of the 5602
CC   nucleotide sequences defined in the specification, where the
CC   oligonucleotide comprises at least 15 nucleotides; or (b) a combination
CC   of an oligonucleotide comprising a sequence complementary to the
CC   complementary strand of a polynucleotide comprising a sequence complementary to a 5'-end
CC   complementary strand of a polynucleotide which comprises

OM nucleic - nucleic search, using sw model

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                                GenCore version 5.1.6
                                Copyright (c) 1993 - 2005 Compugen Ltd.

Run on:            July 31, 2005, 14:57:07 ; Search time 41.358 Seconds
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Perfect score:   20
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Scoring table:   IDENTITY_NUC
                 Gapop 10.0 , Gapext 1.0

Searched:        1202784 seqs, 81818359 residues

Total number of hits satisfying chosen parameters:    2405568

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
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2	20	100.0	3999	3	US-09-286-891-1	Sequence 1, Appli
3	15.4	77.0	2550	3	US-10-029-180-95	Sequence 95, Appl
4	15.4	77.0	5436	2	US-08-948-277A-2	Sequence 2, Appli
5	15.4	77.0	5436	2	US-09-169-203-2	Sequence 2, Appli
6	15.2	77.0	118143	4	US-09-949-016-17196	Sequence 17196, A
7	15.2	76.0	601	4	US-09-949-016-109435	Sequence 109435,
8	15.2	76.0	601	4	US-09-949-016-109436	Sequence 109436,
9	15.2	76.0	601	4	US-09-949-016-109437	Sequence 109437,
10	15.2	76.0	24395	4	US-09-949-016-14758	Sequence 14758, A
11	15.2	76.0	101835	4	US-09-949-016-14695	Sequence 14695, A
12	15.2	76.0	246444	4	US-09-949-016-13313	Sequence 13313, A
13	14.8	74.0	274	4	US-09-902-540-1290	Sequence 1290, Ap
14	14.8	74.0	339	4	US-09-216-393B-3	Sequence 3, Appli
15	14.8	74.0	601	4	US-09-949-016-72744	Sequence 72744, A
16	14.8	74.0	601	4	US-09-949-016-89850	Sequence 89850, A
17	14.8	74.0	601	4	US-09-949-016-89851	Sequence 89851, A
18	14.8	74.0	601	4	US-09-949-016-181156	Sequence 181156,
19	14.8	74.0	601	4	US-09-949-016-183278	Sequence 183278,
20	14.8	74.0	690	4	US-09-134-000C-1299	Sequence 1299, Ap
21	14.8	74.0	8321	4	US-09-949-016-15013	Sequence 15013, A
22	14.8	74.0	9391	4	US-09-949-016-14299	Sequence 14299, A
23	14.8	74.0	15789	4	US-09-902-540-1139	Sequence 1139, Ap
24	14.8	74.0	21513	4	US-09-949-016-16695	Sequence 16695, A
25	14.8	74.0	21513	4	US-09-949-016-16696	Sequence 16696, A
26	14.8	74.0	21513	4	US-09-949-016-16697	Sequence 16697, A
27	14.8	74.0	53789	4	US-09-949-016-12137	Sequence 12137, A
28	14.8	74.0	53789	4	US-09-949-016-13955	Sequence 13955, A
29	14.8	74.0	82000	4	US-09-949-016-15595	Sequence 15595, A
30	14.8	74.0	83665	4	US-09-949-016-16995	Sequence 16995, A
31	14.8	74.0	94077	4	US-09-949-016-13635	Sequence 13635, A
32	14.8	74.0	228896	4	US-09-949-016-16946	Sequence 16946, A
33	14.8	74.0	111677	3	US-09-949-016-13872	Sequence 13872, A
34	14.8	74.0	137394	4	US-09-949-016-12178	Sequence 12178, A
35	14.8	74.0	137743	4	US-09-949-016-11777	Sequence 11777, A
36	14.8	74.0	140325	4	US-09-949-016-16295	Sequence 16295, A
37	14.8	74.0	140982	4	US-09-949-016-17127	Sequence 17127, A
38	14.8	72.0	504	4	US-09-513-999C-821	Sequence 821, App
39	14.4	72.0	518	3	US-09-221-017B-635	Sequence 635, App
40	14.4	72.0	601	4	US-09-949-016-44914	Sequence 44914, A
41	14.4	72.0	601	4	US-09-949-016-44915	Sequence 44915, A
42	14.4	72.0	819	4	US-09-636-215-571	Sequence 571, App
43	14.4	72.0	819	4	US-09-685-166A-571	Sequence 571, App
44	14.4	72.0	819	4	US-09-679-426-571	Sequence 571, App
45	14.4	72.0	819	4	US-09-759-143-571	Sequence 571, App

ALIGNMENTS

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US-08-971-244-1/c
; Sequence 1, Application US/08971244
; Patent No. 5891719
; Patent No. 5891719
; GENERAL INFORMATION:
;  APPLICANT: Cohen, Lucy
;  APPLICANT: Baeuerle, Patrick
;  TITLE OF INVENTION: IKAP Proteins, Nucleic Acids and Methods
;  NUMBER OF SEQUENCES: 2
;  CORRESPONDENCE ADDRESS:
;  ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
;  STREET: 75 DENISE DRIVE
;  CITY: HILLSBOROUGH
;  STATE: CALIFORNIA
;  COUNTRY: USA
;  ZIP: 94010
;  COMPUTER READABLE FORM:
;  MEDIUM TYPE: Floppy disk
;  COMPUTER: IBM PC compatible
;  OPERATING SYSTEM: PC-DOS/MS-DOS
;  SOFTWARE: Patentin Release #1.0, Version #1.30
;  CURRENT APPLICATION DATA:
;  APPLICATION NUMBER: US/08/971,244
;  FILING DATE:
;  CLASSIFICATION: 435
;  ATTORNEY/AGENT INFORMATION:
;  NAME: OSMAN, RICHARD A
;  REGISTRATION NUMBER: 36,627
;  REFERENCE/DOCKET NUMBER: T97-011
;  TELECOMMUNICATION INFORMATION:
;  TELEPHONE: (650) 343-4341
;  TELEFAX: (650) 343-4342
;  INFORMATION FOR SEQ ID NO: 1:
;  SEQUENCE CHARACTERISTICS:
;  LENGTH: 3999 base pairs
;  TYPE: nucleic acid
;  STRANDEDNESS: double
;  TOPOLOGY: linear
;  MOLECULE TYPE: cDNA
;  FEATURE:
;  NAME/KEY: CDS
;  LOCATION: 1..3996
US-08-971-244-1

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Best Local Similarity   100.0%;  Pred. No. 0.5;
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RESULT 2
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Sequence 1, Application US/09286891
Patent No. 6172195
GENERAL INFORMATION:
;   APPLICANT: Cohen, Lucy
;   APPLICANT: Baeuerle, Patrick
;   TITLE OF INVENTION: IKAP Proteins, Nucleic Acids and Methods
;   NUMBER OF SEQUENCES: 2
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
;   STREET: 75 DENISE DRIVE
;   CITY: HILLSBOROUGH
;   STATE: CALIFORNIA
;   COUNTRY: USA
;   ZIP: 94010
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: Patentin Release #1.0, Version #1.30
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/09/286,891
;   FILING DATE:
;   CLASSIFICATION:
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: 08/971,244
;   FILING DATE:
;   ATTORNEY/AGENT INFORMATION:
;   NAME: OSMAN, RICHARD A
;   REGISTRATION NUMBER: 36,627
;   REFERENCE/DOCKET NUMBER: T97-011
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE: (650) 343-4341
;   TELEFAX: (650) 343-4342
;   INFORMATION FOR SEQ ID NO: 1:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 3999 base pairs
;   TYPE: nucleic acid
;   STRANDEDNESS: double
;   TOPOLOGY: linear
;   MOLECULE TYPE: cDNA
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: 1..3996
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; US-09-286-891-1

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Best Local Similarity 100.0%;
Matches 20;   Conservative   0;   Pred. No. 0.5;   Mismatches 0;   Indels 0;   Gaps 0;

RESULT 3
US-10-029-180-95
Sequence 95, Application US/10029180
Patent No. 6806082
GENERAL INFORMATION:
;   APPLICANT: Cali, Brian M.
;   APPLICANT: Holtzman, Doug
;   APPLICANT: Madden, Kevin T.
;   APPLICANT: Milne, G. Todd
;   APPLICANT: Sherman, Amir
;   APPLICANT: Silva, Jeffry C.
;   APPLICANT: Trueheart, Josh
;   APPLICANT: Zhang, Lixin
;   TITLE OF INVENTION: No. 68060e2el Regulators of Fungal Gene Expression

;   FILE REFERENCE: MIC-004
;   CURRENT APPLICATION NUMBER: US/10/029,180
;   CURRENT FILING DATE: 2001-12-22
;   PRIOR APPLICATION NUMBER: US 60/257,431
;   PRIOR FILING DATE: 2000-12-22
;   NUMBER OF SEQ ID NOS: 138
;   SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 95
;   LENGTH: 2550
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: fungal gene
; US-10-029-180-95

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Db 878 TGCTCTCATAGCATCGC 894

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RESULT 4
US-08-948-277A-2
Sequence 2, Application US/08948277A
Patent No. 5849581
GENERAL INFORMATION:
;   APPLICANT: Amaral, M. Catherine
;   APPLICANT: Zhang, Ning
;   APPLICANT: Chen, Jin-Long
;   TITLE OF INVENTION: Regulators of UCP3 Gene Expression
;   NUMBER OF SEQUENCES: 2
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
;   STREET: 75 DENISE DRIVE
;   CITY: HILLSBOROUGH
;   STATE: CALIFORNIA
;   COUNTRY: USA
;   ZIP: 94010
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: Patentin Release #1.0, Version #1.30
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/08/948,277A
;   FILING DATE:
;   CLASSIFICATION: 435
;   ATTORNEY/AGENT INFORMATION:
;   NAME: OSMAN, RICHARD A
;   REGISTRATION NUMBER: 36,627
;   REFERENCE/DOCKET NUMBER: T97-009
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE: (650) 343-4341
;   TELEFAX: (650) 343-4342
;   INFORMATION FOR SEQ ID NO: 2:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 5436 base pairs
;   TYPE: nucleic acid
;   STRANDEDNESS: double
;   TOPOLOGY: linear
;   MOLECULE TYPE: DNA (genomic)
; US-08-948-277A-2

Qy   2 ACTGCGCTCATAGCATC 18
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Db 256 ACTGGTCTCATAGCATC 272

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Best Local Similarity 94.1%;
Matches 16;   Conservative   0;   Pred. No. 1.7e+02;   Mismatches 1;   Indels 0;   Gaps 0;

OM nucleic - nucleic search, using sw model

GenCore version 5.1.6
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Run on: July 31, 2005, 16:38:33 ; Search time 204.198 Seconds
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9: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq:*
10: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq:*
11: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*
12: /cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq:*
13: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:*
14: /cgn2_6/ptodata/1/pubpna/US09_PUBCOMB.seq:*
15: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*
16: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq:*
17: /cgn2_6/ptodata/1/pubpna/US10D_PUBCOMB.seq:*
18: /cgn2_6/ptodata/1/pubpna/US10F_PUBCOMB.seq:*
19: /cgn2_6/ptodata/1/pubpna/US10G_PUBCOMB.seq:*
20: /cgn2_6/ptodata/1/pubpna/US10I_PUBCOMB.seq:*
21: /cgn2_6/ptodata/1/pubpna/US10H_PUBCOMB.seq:*
22: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq:*
23: /cgn2_6/ptodata/1/pubpna/US11_PUBCOMB.seq:*
24: /cgn2_6/ptodata/1/pubpna/US11A_PUBCOMB.seq:*
25: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*
26: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	20	100.0	20	13	US-10-041-856-84	Sequence 84, Appl
2	20	100.0	20	20	US-10-719-993-4494	Sequence 4494, Ap
3	20	100.0	201	20	US-10-719-993-4508	Sequence 4508, Ap
4	20	100.0	201	20	US-10-719-993-4509	Sequence 4509, Ap
5	20	100.0	201	20	US-10-719-993-4523	Sequence 4523, Ap
6	20	100.0	201	20	US-10-719-993-4535	Sequence 4535, Ap
7	20	100.0	201	20	US-10-719-993-4536	Sequence 4536, Ap
8	20	100.0	201	20	US-10-719-993-4551	Sequence 4551, Ap
9	20	100.0	201	20	US-10-719-993-4564	Sequence 4564, Ap
10	20	100.0	201	20	US-10-719-993-4565	Sequence 4565, Ap
11	20	100.0	201	20	US-10-719-993-4580	Sequence 4580, Ap
12	20	100.0	201	20	US-10-719-993-4593	Sequence 4593, A
13	20	100.0	201	20	US-10-719-993-4594	Sequence 4594, Ap
14	20	100.0	201	20	US-10-719-993-4609	Sequence 4609, Ap
15	20	100.0	201	20	US-10-719-993-4621	Sequence 4621, Ap
16	20	100.0	201	20	US-10-719-993-4622	Sequence 4622, Ap
17	20	100.0	201	20	US-10-719-993-34845	Sequence 34845, A
18	20	100.0	201	20	US-10-719-993-34844	Sequence 34844, A
19	20	100.0	201	20	US-10-719-993-319	Sequence 319, App
20	20	100.0	4256	10	US-09-930-113-276	Sequence 276, App
21	20	100.0	4803	21	US-10-719-993-1094	Sequence 1094, Ap
22	20	100.0	5840	13	US-10-719-993-322	Sequence 322, App
23	20	100.0	5924	13	US-10-719-993-320	Sequence 320, Appli
24	20	100.0	5957	20	US-10-719-993-321	Sequence 321, App
25	20	100.0	6107	20	US-10-719-993-318	Sequence 318, Appli
26	20	100.0	6179	13	US-10-719-993-6863	Sequence 6863, Ap
27	20	100.0	66479	13	US-10-041-856-1	Sequence 1, Appli
28	20	100.0	78878	13	US-10-719-956-141010	Sequence 141010,
29	16.4	82.0	25	22	US-09-795-686-1453	Sequence 1453, Ap
30	15.8	79.0	405	9	US-09-795-686-1453	Sequence 1453, Ap
31	15.8	79.0	405	9	US-09-795-686-1453	Sequence 1453, Ap
32	15.8	79.0	405	9	US-10-437-963-43775	Sequence 43775, A
33	15.8	79.0	435	19	US-10-027-632-39553	Sequence 39553, A
34	15.8	79.0	435	13	US-10-027-632-39553	Sequence 39553, A
35	15.8	79.0	587	13	US-10-027-632-314335	Sequence 314335,
36	15.8	79.0	587	13	US-10-027-632-314336	Sequence 314336,
37	15.8	79.0	587	17	US-10-027-632-39553	Sequence 39553, A
38	15.8	79.0	587	17	US-10-027-632-314335	Sequence 314335,
39	15.8	79.0	587	17	US-10-027-632-314336	Sequence 314336,
40	15.8	79.0	1016	19	US-10-437-963-30748	Sequence 30748, A
41	15.8	79.0	29944	21	US-10-437-963-30748	Sequence 30748, A
42	15.8	79.0	51615	21	US-10-468-326-3	Sequence 3, Appli
43	15.8	79.0	81615	19	US-10-087-192-1972	Sequence 1972, Ap
44	15.8	79.0	81924	19	US-10-741-601-5636	Sequence 5636, Ap
45	15.8	79.0	180227	19	US-10-322-281-308	Sequence 308, App
	15.8	79.0	1503641	9	US-09-795-668-1	Sequence 1, Appli

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

ALIGNMENTS

RESULT 1
US-10-041-856-84
Sequence 84, Application US/10041856
Publication No. US20020169299A1
GENERAL INFORMATION:
APPLICANT: SLAUGENHAUPT, SUSAN
APPLICANT: GUSELLA, JAMES F.
TITLE OF INVENTION: GENE FOR IDENTIFYING INDIVIDUALS WITH FAMILIAL
TITLE OF INVENTION: DYSAUTONOMIA
FILE REFERENCE: 1829-4004US1
CURRENT APPLICATION NUMBER: US/10/041,856
CURRENT FILING DATE: 2002-07-08
PRIOR APPLICATION NUMBER: 60/260,080
PRIOR FILING DATE: 2001-01-06
NUMBER OF SEQ ID NOS: 88
SOFTWARE: PatentIn Ver. 2.1
US-10-041-856-84

SEQ ID NO 84
LENGTH: 20
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Primer
US-10-041-856-84

Query Match 100.0%; Score 20; DB 13; Length 20;
Best Local Similarity 100.0%;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GACTGCTCTCATAGCATCGC 20
|||||||||||||||||||||
1 GACTGCTCTCATAGCATCGC 20

Db   1 GACTGCTCTCATAGCATCGC 20

RESULT 2
US-10-719-993-4494/c
; Sequence 4494, Application US/10719993
; Publication No. US20040265849A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: ALZHEIMER'S DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001496
; CURRENT APPLICATION NUMBER: US/10/719,993
; CURRENT FILING DATE: 2003-11-24
; NUMBER OF SEQ ID NOS: 55342
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 4494
; LENGTH: 201
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-719-993-4494

Query Match   100.0%; Score 20; DB 20; Length 201;
Best Local Similarity 100.0%; Pred. No. 2.8;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy   1 GACTGCTCTCATAGCATCGC 20
              ||||||||||||||||||||
Db   34 GACTGCTCTCATAGCATCGC 15

RESULT 3
US-10-719-993-4508/c
; Sequence 4508, Application US/10719993
; Publication No. US20040265849A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: ALZHEIMER'S DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001496
; CURRENT APPLICATION NUMBER: US/10/719,993
; CURRENT FILING DATE: 2003-11-24
; NUMBER OF SEQ ID NOS: 55342
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 4508
; LENGTH: 201
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-719-993-4508

Query Match   100.0%; Score 20; DB 20; Length 201;
Best Local Similarity 100.0%; Pred. No. 2.8;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy   1 GACTGCTCTCATAGCATCGC 20
              ||||||||||||||||||||
Db   34 GACTGCTCTCATAGCATCGC 15

RESULT 4
US-10-719-993-4509/c
; Sequence 4509, Application US/10719993
; Publication No. US20040265849A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: ALZHEIMER'S DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001496
; CURRENT APPLICATION NUMBER: US/10/719,993
; CURRENT FILING DATE: 2003-11-24
; NUMBER OF SEQ ID NOS: 55342
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 4509

; LENGTH: 201
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-719-993-4509

Query Match   100.0%; Score 20; DB 20; Length 201;
Best Local Similarity 100.0%; Pred. No. 2.8;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy   1 GACTGCTCTCATAGCATCGC 20
              ||||||||||||||||||||
Db   89 GACTGCTCTCATAGCATCGC 70

RESULT 5
US-10-719-993-4523/c
; Sequence 4523, Application US/10719993
; Publication No. US20040265849A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: ALZHEIMER'S DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001496
; CURRENT APPLICATION NUMBER: US/10/719,993
; CURRENT FILING DATE: 2003-11-24
; NUMBER OF SEQ ID NOS: 55342
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 4523
; LENGTH: 201
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-719-993-4523

Query Match   100.0%; Score 20; DB 20; Length 201;
Best Local Similarity 100.0%; Pred. No. 2.8;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy   1 GACTGCTCTCATAGCATCGC 20
              ||||||||||||||||||||
Db   34 GACTGCTCTCATAGCATCGC 15

RESULT 6
US-10-719-993-4535/c
; Sequence 4535, Application US/10719993
; Publication No. US20040265849A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: ALZHEIMER'S DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001496
; CURRENT APPLICATION NUMBER: US/10/719,993
; CURRENT FILING DATE: 2003-11-24
; NUMBER OF SEQ ID NOS: 55342
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 4535
; LENGTH: 201
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-719-993-4535

Query Match   100.0%; Score 20; DB 20; Length 201;
Best Local Similarity 100.0%; Pred. No. 2.8;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy   1 GACTGCTCTCATAGCATCGC 20
              ||||||||||||||||||||
Db   133 GACTGCTCTCATAGCATCGC 114

RESULT 7
US-10-719-993-4536/c
; Sequence 4536, Application US/10719993

OM nucleic - nucleic search, using sw model

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

Run on: July 31, 2005, 15:46:58 ; Search time 979.383 Seconds
                                           (without alignments)
                                           777.311 Million cell updates/sec

Title: US-10-041-856-84
Perfect score: 20
Sequence: 1 gactgcctcatagcatcgc 20

Scoring table: IDENTITY_NUC
                 Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   EST.*
                 1: gb_est1:*
                 2: gb_est2:*
                 3: gb_htc:*
                 4: gb_est3:*
                 5: gb_est4:*
                 6: gb_est5:*
                 7: gb_est6:*
                 8: gb_gss1:*
                 9: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	Match DB	DB ID	Description
1	20	100.0	231	7	N56173	N56173 J8210F Huma
2	20	100.0	258	7	Z42212	Z42212 HSC0CD041 n
3	20	100.0	380	7	CR788009	CR788009 DKFZp459M
4	20	100.0	492	7	H15327	H15327 Ym28d08.r1
5	20	100.0	529	1	AU127237	AU127237 AU127237
6	20	100.0	550	5	CA397687	CA397687 c994d05.y
7	20	100.0	568	2	AW246917	AW246917 2822633.5
8	20	100.0	583	5	BP311692	BP311692 BP311692
9	20	100.0	603	5	BX478139	BX478139 DKFZp686B
10	20	100.0	766	7	CR789373	CR789373 DKFZp459J
11	20	100.0	793	7	CN256150	CN256150 17000S318
12	20	100.0	803	1	AU124100	AU124100 AU124100
13	20	100.0	828	1	AU124187	AU124187 AU124187
14	20	100.0	849	5	BU935143	BU935143 AGENCOURT
15	20	100.0	853	7	CF552514	CF552514 AGENCOURT
16	20	100.0	866	5	BU508979	BU508979 AGENCOURT
17	20	100.0	868	5	BU856271	BU856271 AGENCOURT
18	20	100.0	874	5	BU156074	BU156074 AGENCOURT
19	20	100.0	885	5	BQ428500	BQ428500 AGENCOURT
20	20	100.0	887	5	BU849172	BU849172 AGENCOURT
21	20	100.0	906	5	BU554148	BU554148 AGENCOURT
22	20	100.0	923	5	BU147179	BU147179 AGENCOURT
23	20	100.0	931	4	BG286503	BG286503 AGENCOURT
24	20	100.0	937	2	BE893879	BE893879 601436245
25	20	100.0	945	5	BU845774	BU845774 AGENCOURT
26	20	100.0	1000	4	BM471267	BM471267 AGENCOURT
27	20	100.0	3833	3	CR749385	CR749385 Homo sapi
28	20	100.0	3999	9	AY414501	AY414501 Homo sapi
29	20	100.0	3999	9	AY414502	AY414502 Pan trogl
30	18.4	92.0	641	5	BQ807986	BQ807986 NISC_kk12
31	18.4	92.0	1134	7	CN641971	CN641971 NISC_kk12
32	18	90.0	1458	9	CL105854	CL105854 ISB1-45M8
33	17.4	87.0	970	8	CC405446	CC405446 PUHCJ22TD
34	17	85.0	818	7	CF752151	CF752151 om_R000.6
35	16.8	84.0	168	7	CV402642	CV402642 601101339
36	16.8	84.0	171	9	BX572126	BX572126 Arabidops
37	16.8	84.0	256	5	BU715404	BU715404 SJMcAE03
38	16.8	84.0	471	2	AW593718	AW593718 hg21e08.x
39	16.8	84.0	556	2	BF582892	BF582892 602101339
40	16.8	84.0	558	4	BG964036	BG964036 602828778
41	16.8	84.0	560	2	BF577636	BF577636 602092511
42	16.8	84.0	560	2	BF584731	BF584731 602098479
43	16.8	84.0	560	2	BF581514	BF581514 602101032
44	16.8	84.0	569	4	BG964537	BG964537 602832211
45	16.8	84.0	577	2	BF583651	BF583651 602101442

ALIGNMENTS

RESULT 1
N56173/c
LOCUS   N56173   231 bp   mRNA   linear   EST 20-FEB-1996
DEFINITION J8210F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA
            clone J8210 5', mRNA sequence.
ACCESSION   N56173
VERSION   N56173.1 GI:1199021
KEYWORDS   EST.
SOURCE   Homo sapiens (human)
  ORGANISM Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 231)
  AUTHORS   Liew,C.C.
  TITLE   cDNAs from fetal heart
  JOURNAL   Unpublished (1995)
COMMENT   Contact: Liew CC
            Harvard Medical School
            Brigham and Women's Hospital
            75 Francis St. Boston, MA 02115, USA
            Tel: 6177328915
            Fax: 6177509995
            Email: cliew@rics.bwh.harvard.edu
            Seq primer: TCCAAAGAATTCGGCACGAG.
FEATURES   Location/Qualifiers
     source   1..231
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="J8210"
                     /lab_host="E. coli Xl1-Blue"
                     /clone_lib="Human fetal heart, Lambda ZAP Express"
                     /note="Vector: Lambda ZAP Express; Site 1: EcoRI; Site_2:
                     XhoI; mRNA was purified from human fetal hearts (8-10
                     week). cDNA was synthesized using a XhoI-Oligo dT
                     adaptor-primer. EcoRI adaptors were ligated, followed by
                     digestion with XhoI, for directional cloning into
                     predigested lambda ZAP Express."
ORIGIN

Query Match   100.0%; Score 20; DB 7; Length 231;
Best Local Similarity   100.0%;
Matches   20; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   1 GACTGCCTCATAGCATCGC 20
              |||||||||||||||||||||
Db   144 GACTGCCTCATAGCATCGC 125

RESULT 2
LOCUS   Z42212/c
DEFINITION   Z42212   258 bp   mRNA   linear   EST 08-NOV-1994
             HSC0CD041 normalized infant brain cDNA Homo sapiens cDNA clone
             C-0cd04, mRNA sequence.
ACCESSION   Z42212
VERSION   Z42212.1 GI:565316
KEYWORDS   EST.
SOURCE   Homo sapiens (human)
  ORGANISM   Homo sapiens
             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
             Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 258)
  AUTHORS   Auffray,C., Behar,G., Bois,F., Bouchier,C., da Silva,C.,
             Devignes,M.D., Duprat,S., Houlgatte,R., Jumeau,M.N., Lamy,B.,
             Lorenzo,F., Mitchell,H., Mariage-Samson,R., Pietu,G., Pouliot,Y.,
             Sebastiani-Kabaktchis,C. and Tessier,A.
  TITLE   IMAGE: molecular integration of the analysis of the human genome
             and its expression
  JOURNAL   C. R. Acad. Sci. III, Sci. Vie 318 (2), 263-272 (1995)
   MEDLINE   95527534
   PUBMED   7557816
COMMENT   Contact: Genethon
             Genexpress-Genethon
             Genethon Centre de recherche sur le Genome Humain
             1,rue de l'Internationale, BP60 91002 EVRY Cedex, FRANCE
             Tel: 3316947280O
             Fax: 3316O778698
             Email: Genexpress@genethon.fr
             Single read.
             Genexpress_library_idt: C; Genexpress_sequence_idt: y1c-0cd04
             Seq primer: (-21)M13 universal.
FEATURES   Location/Qualifiers
     source   1..258
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="C-0cd04"
                     /sex="Female"
                     /tissue_type="total brain"
                     /clone_lib="normalized infant brain cDNA"
                     /note="Organ: brain; Vector: lafmid BA; Site_1: HindIII;
                     Site_2: NotI; sex=Female; dev_stage=3 months old;
                     isolate=muscular atrophy patient; tissue_type=total
                     brain; total mRNA was oligo-(dT) primed and directionally
                     cloned 5'-> 3' into the HindIII -> NotI sites of the
                     lafmid BA vector. Clone library from B.Soares,
                     Dept. Columbia University, USA. Normalization_method:
                     Bento Soares, P.N.A.S in press"
ORIGIN
Query Match   100.0%;   Score 20;   DB 7;   Length 258;
Best Local Similarity   100.0%;   Pred. No. 16;
Matches 20;   Conservative   0;   Mismatches   0;   Indels   0;   Gaps   0;

Qy   1 GACTGCTCTCATAGCATCGC 20
        ||||||||||||||||||||
Db 205 GACTGCTCTCATAGCATCGC 186

RESULT 3
LOCUS   CR788009/c
DEFINITION   CR788009   380 bp   mRNA   linear   EST 01-OCT-2004
             DKFZp459M2022_r1 459 (synonym: pcor1) Pongo pygmaeus cDNA clone
             DKFZp459M2022_5', mRNA sequence.
ACCESSION   CR788009
VERSION   CR788009.1 GI:53707006
KEYWORDS   EST.
SOURCE   Pongo pygmaeus (orangutan)
  ORGANISM   Pongo pygmaeus

REFERENCE   1 (bases 1 to 380)
  AUTHORS   Ottenwaelder,B., Obermaier,B., Deutschenbaur,S., Schalpp,A.,
             Mewes,H.W., Weil,B., Amid,C., Osanger,A., Fobo,G., Han,M. and
             Wiemann,S.
  TITLE   Pongo pygmaeus mRNA (Ottenwaelder,B., Obermaier,B.,
             Deutschenbaur,S., et al.)
  JOURNAL   Unpublished (2004)
COMMENT   Contact: MIPS
             MIPS
             Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany
             This is the 5' sequence of the clone insert. Clone from S. Wiemann,
             Molecular Genome Analysis, German Cancer Research Center (DKFZ);
             Email s.wiemann@dkfz-heidelberg.de; sequenced by Medigenomix
             (Martinsried/Germany) within the cDNA sequencing consortium of the
             German Genome Project. This clone (DKFZp459M2022) is available at
             the RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH in
             Berlin, Germany. Please contact RZPD for ordering.
             http://www.rzpd.de/cgi-bin/products/cl.cgi?CloneID=DKFZp459M2022
             Further information about the clone and the sequencing project is
             available at http://mips.gsf.de/projects/cdna/.
FEATURES   Location/Qualifiers
     source   1..380
                     /organism="Pongo pygmaeus"
                     /mol_type="mRNA"
                     /db_xref="taxon:9600"
                     /clone="DKFZp459M2022"
                     /tissue_type="cortex"
                     /dev_stage="adult"
                     /lab_host="DH10B"
                     /clone_lib="459 (synonym: pcor1)"
                     /note="Vector: pSport1_Sfi; Site_1: SfiIA; Site_2: SfiIB"
ORIGIN
Query Match   100.0%;   Score 20;   DB 7;   Length 380;
Best Local Similarity   100.0%;   Pred. No. 17;
Matches 20;   Conservative   0;   Mismatches   0;   Indels   0;   Gaps   0;

Qy   1 GACTGCTCTCATAGCATCGC 20
        ||||||||||||||||||||
Db 294 GACTGCTCTCATAGCATCGC 275

RESULT 4
LOCUS   H15327/c
DEFINITION   H15327   492 bp   mRNA   linear   EST 27-JUN-1995
             ym28d08.r1 Soares infant brain 1NIB Homo sapiens cDNA clone
             IMAGE:49526 5', mRNA sequence.
ACCESSION   H15327
VERSION   H15327.1 GI:880147
KEYWORDS   EST.
SOURCE   Homo sapiens (human)
  ORGANISM   Homo sapiens
             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
             Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 492)
  AUTHORS   Hillier,L., Clark,N., Dubnick,T., Elliston,K., Hawkins,M.,
             Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
             Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
             Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
             Wilson,R.
  TITLE   The WashU-Merck EST Project
  JOURNAL   Unpublished (1995)
COMMENT   Contact: Wilson RK
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             Tel: 314 286 1800
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             Email: est@watson.wustl.edu
             Insert Size: 2471
             High quality sequence stops: 367
             Source: IMAGE Consortium, LLNL